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(54) Title: ENDOTHELIAL CELL EXPRESSION PATTERNS

(57) Abstract: To gain a better understanding of tumor angiogenesis, new techniques for isolating endothelial cells (ECs) and evaluating gene expression patterns were developed. When transcripts from ECs derived from normal and malignant colorectal tissues were compared with transcripts from non-endothelial cells, over 170 genes predominantly expressed in the endothelium were identified. Comparison between normal- and tumor-derived endothelium revealed 79 differentially expressed genes, including 46 that were specifically elevated in tumor-associated endothelium. Experiments with representative genes from this group demonstrated that most were similarly expressed in the endothelium of primary lung, breast, brain, and pancreatic cancers as well as in metastatic lesions of the liver. These results demonstrate that neoplastic and normal endothelium in humans are distinct at the molecular level, and have significant implications for the development of anti-angiogenic therapies in the future.

ENDOTHELIAL CELL EXPRESSION PATTERNS

- [01] This application claims the benefit of provisional applications serial numbers 60/222,599 filed August 2, 2000, 60/224,360 filed August 11, 2000, and 60/282,850 filed April 11, 2001, the disclosures of which are expressly incorporated herein.
- [02] The U.S. government retains certain rights in the invention by virtue of the provisions of National Institutes of Health grants CA57345 and CA43460, which supported this work.

TECHNICAL FIELD OF THE INVENTION

- [03] This invention is related to the area of angiogenesis and anti-angiogenesis. In particular, it relates to genes which are characteristically expressed in tumor endothelial and normal endothelial cells.

BACKGROUND OF THE INVENTION

- [04] It is now widely recognized that tumors require a blood supply for expansive growth. This recognition has stimulated a profusion of research on tumor angiogenesis, based on the idea that the vasculature in tumors represents a potential therapeutic target. However, several basic questions about tumor endothelium remain unanswered. For example, are vessels of tumors qualitatively different from normal vessels of the same tissue? What is the relationship of tumor endothelium to endothelium of healing wounds or other physiological or pathological forms of angiogenesis? The answers to these questions critically impact on the potential for new therapeutic approaches to inhibit angiogenesis in a specific manner.

[05] There is a continuing need in the art to characterize the vasculature of tumors relative to normal vasculature so that any differences can be exploited for therapeutic and diagnostic benefits.

[06] One technique which can be used to characterize gene expression, or more precisely gene transcription, is termed serial analysis of gene expression (SAGE). Briefly, the SAGE approach is a method for the rapid quantitative and qualitative analysis of mRNA transcripts based upon the isolation and analysis of short defined sequence tags (SAGE Tags) corresponding to expressed genes. Each Tag is a short nucleotide sequences (9-17 base pairs in length) from a defined position in the transcript. In the SAGE method, the Tags are dimerized to reduce bias inherent in cloning or amplification reactions. (See, US Patent 5,695,937) SAGE is particularly suited to the characterization of genes associated with vasculature stimulation or inhibition because it is capable of detecting rare sequences, evaluating large numbers of sequences at one time, and to provide a basis for the identification of previously unknown genes.

SUMMARY OF THE INVENTION

[07] One embodiment of the invention provides an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 17, 19, and 44, as shown in SEQ ID NO: 196, 200, 212, 230, 232, and 271, respectively. The molecule can be, for example, an intact antibody molecule, a single chain variable region (ScFv), a monoclonal antibody, a humanized antibody, or a human antibody. The molecule can optionally be bound to a cytotoxic moiety, bound to a therapeutic moiety, bound to a detectable moiety, or bound to an anti-tumor agent.

[08] According to another embodiment of the invention a method of inhibiting neoangiogenesis is provided. An effective amount of an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 17, 19, 22, and 44, as shown in SEQ ID NO: 196, 200, 212, 230, 232, 238, and 271, respectively, is administered to a subject in need thereof. Neoangiogenesis is consequently inhibited. The subject may bear a vascularized tumor, may have polycystic kidney disease, may have diabetic retinopathy, may have rheumatoid arthritis, may have psoriasis, for example.

[09] Another aspect of the invention is a method of inhibiting tumor growth. An effective amount of an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 17, 19, 22, and 44, as shown in SEQ ID NO: 196, 200, 212, 230, 232, 238, and 271, respectively, is administered to a human subject bearing a tumor. The growth of the tumor is consequently inhibited.

[10] Still another aspect of the invention provides an isolated molecule comprising an antibody variable region which specifically binds to a TEM protein selected from the group consisting of: 3, 9, 17, 19, and 44, as shown in SEQ ID NO: 200, 212, 230, 232, and 271 , respectively. The molecule can be, for example, an intact antibody molecule, a single chain variable region (ScFv), a monoclonal antibody, a humanized antibody, or a human antibody. The molecule can optionally be bound to a cytotoxic moiety, bound to a therapeutic moiety, bound to a detectable moiety, or bound to an anti-tumor agent.

[11] According to still another aspect of the invention an isolated and purified human transmembrane protein is provided. The protein is selected from the group consisting of: TEM 3, 9, 17, and 19 as shown in SEQ ID NO: 200, 212, 230, and 232, respectively.

[12] Yet another aspect of the invention is an isolated and purified nucleic acid molecule comprising a coding sequence for a transmembrane TEM selected from the group consisting of: : TEM 3, 9, 17, and 19 as shown in SEQ ID NO: 200, 212, 230, and 232, respectively. The isolated and purified nucleic acid molecule may optionally comprise a coding sequence selected from those shown in SEQ ID NO: : 199, 211, 229, and 231.

[13] Still another aspect of the invention is a recombinant host cell which comprises a nucleic acid molecule. The nucleic acid molecule comprises a coding sequence for a transmembrane TEM selected from the group consisting of: : TEM 3, 9, 17, and 19 as shown in SEQ ID NO: 200, 212, 230, and 232, respectively. The recombinant host cell optionally comprises a coding sequence selected from those shown in SEQ ID NO: 199, 211, 229, and 231.

[14] According to one embodiment of the invention a method is provided for inducing an immune response in a mammal. A nucleic acid molecule comprising a coding sequence for a human transmembrane protein selected from the group consisting of: TEM 1, 3, 9, 13, 17, 19, 22, 30, and 44 as shown in SEQ ID NO: , respectively, is administered to the mammal. An immune response to the human transmembrane protein is thereby induced in the mammal. Optionally the coding sequence is shown in SEQ ID NO: 196, 200, 212, 220, 230, 232, 238, 250 and 271.

[15] According to yet another embodiment of the invention a method of inducing an immune response in a mammal is provided. A purified human transmembrane protein selected from the group consisting of: TEM 1, 3, 9, 13, 17, 19, 22, 30, and 44 as shown in SEQ ID NO: 196, 200, 212, 220, 230, 232, 238, 250 and 271, respectively, is administered to the mammal. An immune response to the human transmembrane protein is thereby induced in the mammal.

[16] Another aspect of the invention is a method for identification of a ligand involved in endothelial cell regulation. A test compound is contacted with an isolated and purified human transmembrane protein selected from the group consisting of 1, 3, 9, 13, 17, 30, 19, and 44 as shown in SEQ ID NO: 196, 200, 212, 220, 230, 232, 250, and 271. The isolated and purified human transmembrane protein is also contacted with a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 13, 17, 30, 19, and 44 as shown in SEQ ID NO: 196, 200, 212, 220, 230, 232, 250, and 271 respectively. Binding of the molecule comprising an antibody variable region to the human transmembrane protein is determined. A test compound which diminishes the binding of the molecule comprising an antibody variable region to the human transmembrane protein is identified as a ligand involved in endothelial cell regulation.

[17] Yet another aspect of the invention is a method for identification of a ligand involved in endothelial cell regulation. A test compound is contacted with a cell comprising a human transmembrane protein selected from the group consisting of 1, 3, 9, 17, and 19 as shown in SEQ ID NO: 196, 200, 212, 230, and 232. The cell is also contacted with a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 17, and 19 as shown in SEQ ID NO: 196, 200, 212, 230, and 232 , respectively. Binding of the molecule comprising an antibody variable region to the cell is determined. A test compound which diminishes the binding of the molecule comprising an antibody variable region to the cell is identified as a ligand involved in endothelial cell regulation.

[18] Yet another aspect of the invention is a method for identification of a ligand involved in endothelial cell regulation. A test compound is contacted with a human transmembrane protein selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27,

28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275. Binding of a test compound to the human transmembrane protein is determined. A test compound which binds to the protein is identified as a ligand involved in endothelial cell regulation.

[19] Another embodiment of the present invention is a soluble form of a human transmembrane protein selected from the group consisting of: TEM 1, 3, 9, 17, 19, 22, 30, and 44 as shown in SEQ ID NO: 196, 200, 212, 230, 232, 238, 250, and 271 respectively. The soluble forms lack transmembrane domains. The soluble form may consist of an extracellular domain of the human transmembrane protein.

[20] Also provided by the present invention is a method of inhibiting neoangiogenesis in a patient. A soluble form of a human transmembrane protein is administered to the patient. Neoangiogenesis in the patient is consequently inhibited. The patient may bear a vascularized tumor, may have polycystic kidney disease, may have diabetic retinopathy, may have rheumatoid arthritis, or may have psoriasis, for example.

[21] Another embodiment of the invention provides a method of inhibiting neoangiogenesis in a patient. A soluble form of a human transmembrane protein is administered to the patient. Neoangiogenesis in the patient is consequently inhibited. The patient may bear a vascularized tumor, may have polycystic kidney disease, may have diabetic retinopathy, may have rheumatoid arthritis, or may have psoriasis, for example.

[22] According to still another aspect of the invention a method of identifying regions of neoangiogenesis in a patient is provided. A molecule comprising an antibody variable region which specifically binds to an

extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 13, 17, 19, 22, 30, and 44, as shown in SEQ ID NO: 196, 200, 212, 220, 230, 232, 238, 250, and 271, respectively, is administered to a patient. The molecule is bound to a detectable moiety. The detectable moiety is detected in the patient, thereby identifying neoangiogenesis.

[23] According to another aspect of the invention a method is provided for inducing an immune response to tumor endothelial cells in a patient. A mouse TEM protein selected from the group consisting of: 1, 2, 3, 9, 13, 17, 19, 22, and 30 as shown in SEQ ID NO: 291, 293, 299, 295, 303, 297, 301, 305, and 307, is administered to a patient in need thereof. An immune response to a human TEM protein is consequently induced.

[24] Still another embodiment of the invention is a method of screening for neoangiogenesis in a patient. A body fluid collected from the patient is contacted with a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 17, 19, and 44, as shown in SEQ ID NO: 196, 200, 212, 230, 232, and 271, respectively. Detection of cross-reactive material in the body fluid with the molecule indicates neo-angiogenesis in the patient.

[25] Still another embodiment of the invention provides a method of inhibiting neoangiogenesis in a patient. A molecule comprising an antibody variable region which specifically binds to a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40 as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 and 224, 234, 242, 244, 252, 257, 259, 261, 263, and 265, is administered to the patient. Neoangiogenesis in the patient consequently inhibited.

[26] Yet another aspect of the invention is a method of screening for neoangiogenesis in a patient. A body fluid collected from the patient is

contacted with a molecule comprising an antibody variable region which specifically binds to a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 234, 242, 244, 252, 257, 259, 261, 263, and 265, respectively. Detection of cross-reactive material in the body fluid with the molecule indicates neoangiogenesis in the patient.

[27] Also provided by the present invention is a method of promoting neoangiogenesis in a patient. A TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 234, 242, 244, 252, 257, 259, 261, 263, and 265, is administered to a patient in need of neoangiogenesis. Neoangiogenesis in the patient is consequently stimulated.

[28] One embodiment of the invention provides a method of promoting neoangiogenesis in a patient. A nucleic acid molecule encoding a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 201, 205, 207, 213, 217, 221 & 222, 233, 241, 243, 251, 256, 258, 260, 262, and 264, is administered to a patient in need of neoangiogenesis. The TEM protein is consequently expressed and neoangiogenesis in the patient is stimulated.

[29] Another embodiment of the invention provides a method of screening for neoangiogenesis in a patient. A TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 234, 242, 244, 252, 257, 259, 261, 263, and 265, respectively, is detected in a body fluid collected from the patient. Detection of the TEM protein indicates neoangiogenesis in the patient.

[30] Another aspect of the invention is a method of screening for neoangiogenesis in a patient. A nucleic acid encoding a TEM protein

selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40 is detected in a body fluid collected from the patient. The nucleic acid is selected from the group consisting of those shown in SEQ ID NO: 201, 205, 207, 213, 217, 221 & 222, 233, 241, 243, 251, 256, 258, 260, 262, and 264. Detection of the TEM protein indicates neoangiogenesis in the patient.

[31] Yet another embodiment of the invention is an isolated and purified nucleic acid molecule which encodes a NEM protein selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289. The nucleic acid molecule optionally comprises a coding sequence as shown in SEQ ID NO: 278, 282, 284, and 288. The nucleic acid may be maintained in a recombinant host cell.

[32] The present invention also provides an isolated and purified NEM protein selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289.

[33] The present invention further provides an isolated molecule comprising an antibody variable region which specifically binds to a NEM protein selected from the group consisting of: 14, 22, 23, and 33, as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289.

[34] An additional embodiment of the present invention is a method of inhibiting neoangiogenesis. An effective amount of a NEM protein selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289 is administered to a subject in need thereof. Neoangiogenesis is thereby inhibited.

[35] A still further embodiment of the invention is a method to identify candidate drugs for treating tumors. Cells which express one or more TEM genes selected from the group consisting of: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,

12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: : 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 221 & 222, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 256, 258, 260, 262, 266, 268, 270, 272, and 274, respectively, are contacted with a test compound. Expression of said one or more TEM genes is determined by hybridization of mRNA of said cells to a nucleic acid probe which is complementary to said mRNA. A test compound is identified as a candidate drug for treating tumors if it decreases expression of said one or more TEM genes. Optionally the cells are endothelial cells. Alternatively or additionally, the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more TEMs. Test compounds which increase expression can be identified as candidates for promoting wound healing.

[36] Yet another embodiment of the invention is a method to identify candidate drugs for treating tumors. Cells which express one or more TEM proteins selected from the group consisting of: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275, respectively, are contacted with a test compound. The amount of said one or more TEM proteins in said cells is determined. A test compound is identified as a candidate drug for treating tumors if it decreases the amount of one or more TEM proteins in said cells. Optionally the cells are endothelial cells. Alternatively or additionally, the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more TEMs. Alternatively, a test compound which increases the amount of one or more TEM proteins in said cells is identified as a candidate drug for treating wound healing.

[37] According to another aspect of the invention a method is provided to identify candidate drugs for treating tumors. Cells which express one or more TEM proteins selected from the group consisting of: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275, respectively, are contacted with a test compound. Activity of said one or more TEM proteins in said cells is determined. A test compound is identified as a candidate drug for treating tumors if it decreases the activity of one more TEM proteins in said cells. Optionally the cells are endothelial cells. Alternatively or additionally, the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more TEMs. Optionally the cells are endothelial cells. If a test compound increases the acitivity of one more TEM proteins in said cells it can be identified as a candidate drug for treating wound healing.

[38] An additional aspect of the invention is a method to identify candidate drugs for treating patients bearing tumors. A test compound is contacted with recombinant host cells which are transfected with an expression construct which encodes one or more TEM proteins selected from the group consisting of 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275, respectively. Proliferation of said cells is determined. A test compound which inhibits proliferation of said cells is identified as a candidate drug for treating patients bearing tumors. A test compound which stimulates

proliferation of said cells is identified as a candidate drug for promoting neoangiogenesis, such as for use in wound healing.

[39] Another embodiment of the invention provides a method to identify candidate drugs for treating tumors. Cells which express one or more NEM genes selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 278, 282, 284, and 288, respectively, are contacted with a test compound. Expression of said one or more NEM genes is determined by hybridization of mRNA of said cells to a nucleic acid probe which is complementary to said mRNA. A test compound is identified as a candidate drug for treating tumors if it increases expression of said one or more NEM genes. Optionally the cells are endothelial cells. Alternatively or additionally, the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more NEMs.

[40] According to another aspect of the invention a method is provided to identify candidate drugs for treating tumors. Cells which express one or more NEM proteins selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, are contacted with a test compound. The amount of said one or more NEM proteins in said cells is determined. A test compound is identified as a candidate drug for treating tumors if it increases the amount of one more NEM proteins in said cells. Optionally the cells are endothelial cells. Alternatively or additionally, the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more NEMs.

[41] An additional aspect of the invention is a method to identify candidate drugs for treating tumors. Cells which express one or more NEM proteins selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, are contacted with a test compound. Activity of said one or more NEM proteins in said cells is determined. A test compound is identified as a candidate drug for treating

tumors if it increases the activity of said one or more NEM proteins in said cells. Optionally the cells are endothelial cells. Alternatively or additionally, the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more NEMs.

[42] Still another embodiment of the invention provides a method to identify candidate drugs for treating patients bearing tumors. A test compound is contacted with recombinant host cells which are transfected with an expression construct which encodes one or more NEM proteins selected from the group consisting of 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289. Proliferation of said cells is determined. A test compound which stimulates proliferation of said cells is identified as a candidate drug for treating patients bearing tumors.

[43] Another aspect of the invention is a method for identifying endothelial cells. One or more antibodies which bind specifically to a TEM or NEM protein selected from the group consisting of TEM : 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 30, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275 and NEM 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, is contacted with a population of cells. Cells in the population which have bound to said antibodies are detected. Cells which are bound to said antibodies are identified as endothelial cells. Optionally cells which have bound to said antibodies are isolated from cells which have not bound.

[44] Still another aspect of the invention is a method for identifying endothelial cells. One or more nucleic acid hybridization probes which are complementary to a TEM or NEM gene nucleic acid sequence selected from the group consisting of of TEM : 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16,

17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 30, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275 and NEM 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, is contacted with nucleic acids of a population of cells. Nucleic acids which have specifically hybridized to said nucleic acid hybridization probes are detected. Cells whose nucleic acids specifically hybridized are identified as endothelial cells.

[45] Yet another embodiment of the invention is a method of inhibiting neoangiogenesis. An effective amount of an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a mouse TEM protein selected from the group consisting of: 1, 2, 3, 9, 17, and 19, as shown in SEQ ID NO: 291, 293, 299, 295, 297, and 301, respectively, is administered to a subject in need thereof. Neoangiogenesis is thereby inhibited. The subject may be a mouse, may bear a vascularized tumor, may have polycystic kidney disease, may have diabetic retinopathy, may have rheumatoid arthritis, or may have psoriasis, for example.

[46] These and other embodiments which will be apparent to those of skill in the art upon reading the specification provide the art with reagents and methods for detection, diagnosis, therapy, and drug screening pertaining to neoangiogenesis and pathological processes involving or requiring neoangiogenesis.

BRIEF DESCRIPTION OF THE DRAWINGS

[47] Fig. 1A-1B. vWF expression in colorectal cancers. vWF (red stain) was detected in vessels by *in situ* hybridization. At low power magnification (Fig. 1.A) vessels were often surrounded by a perivascular cuff of viable cells

(red arrows), with a ring of necrotic cells evident at the periphery (black arrows). At high power magnification (Fig. 1.B) the expression of vWF (red) was clearly localized to the vessels. Sections were counterstained with methyl green.

[48] Fig. 2A-2D. Purification of Endothelial Cells (ECs) from human normal and malignant tissue. (Fig. 2A) Vessels (red) of frozen sections were stained by immunofluorescence with the P1H12 monoclonal antibody (Chemicon, Temecula, CA) and detected using a biotinylated goat anti-mouse IgG secondary antibody followed by rhodamine-linked strepavidin. The region stained is from within the lamina propria of normal colonic mucosa. Note that the larger vessels (arrowheads) and capillaries (arrows) are positive, and staining of hematopoietic cells was undetectable. E-cadherin positive epithelial cells (green) at the edge of the crypt were simultaneously visualized using a rabbit polyclonal antibody (Santa Cruz, Santa Cruz, CA), followed by a goat anti-rabbit IgG secondary antibody labelled with alexa (Molecular Probes, Eugene, OR). Sections were imaged at 60X magnification using confocal microscopy. (Fig. 2.B) To isolate pure populations from collagenase dispersed tissues, the epithelial and hematopoietic cell fractions were sequentially removed by negative selection with magnetic beads. The remaining cells were stained with P1H12 and ECs were isolated by positive selection with magnetic beads. (Fig. 2.C) RT-PCR analysis used to assess the purity of the EC preparations. Semiquantitative PCR analysis was performed on cDNA generated either directly from colorectal cancer tissue (unfractionated tumor) or from purified ECs isolated from normal colonic mucosa (normal EC fraction) or colorectal cancer (tumor EC fraction). PCR amplification of the epithelial specific marker cytokeratin 20 (CK20), demonstrated its expression was limited to the unfractionated tumor. Two endothelial specific markers, vWF and VE-cadherin (VE-Cad) showed robust amplification only in the endothelial fractions, validating the purity and enrichment protocol shown in (Fig. 2.B). The ubiquitous housekeeping enzyme GAPDH was observed in all samples.

No signal was detected in the no-template (NT) control. cDNA templates were diluted 1:10, 1:100, 1:1000, 1:4000, and 1:40,000 as indicated by the declining wedge. (Fig. 2.D) The relative expression level of select genes was determined by measuring the tag abundance from several SAGE libraries combined into four groups. The first was composed of ~193,000 tags from the two *in vivo*-derived EC preparations (Endothelial Cell Fraction) while the second contained a single library of ~57,000 tags containing macrophages and other leukocytes derived from the negative selection (Hematopoietic Fraction). The fourth library contained ~401,000 tags from cultured HUVEC and HMVEC (Endothelial Cells in Culture), and the fourth consisted of ~748,000 tags from 6 colon cancer cell lines in culture (Epithelial Cells). After normalization, the library with the highest tag number for each marker was given a value of 100%, and the corresponding relative expression levels of the remaining 3 libraries was plotted on the ordinate. Note the high level of CD31 present on hematopoietic cells, the likely cause of the impurity of the initial endothelial selection, compared with the selectivity of P1H12.

[49] Fig. 3A- 3E). Expression of Pan-Endothelial Markers (PEMs) is limited to ECs. The endothelial origin of PEMs identified by SAGE was confirmed using a highly sensitive *in situ* hybridization assay. Localization of novel PEMs to the ECs was demonstrated by examining two representative PEMs, PEM3 (Fig. 3A) and PEM6 (Fig. 3B) in lung cancer and colon cancer, respectively. Hevin expression was readily detected in the ECs of a colon tumor (Fig. 3C) despite its low level of expression in cultured ECs. Expression of VEGFR2 was readily detectable in the ECs of both normal (Fig. 3D) and malignant colon tissue (Fig. 3E).

[50] Fig. 4A-4J. Expression of Tumor Endothelial Markers (TEMs). (Fig. 4A) RT-PCR analysis confirmed the tumor specific expression of selected novel TEMs. Semiquantitative PCR analysis was performed on cDNA generated either from purified epithelial cells as a negative control (Control) or from purified ECs isolated from normal colonic mucosa (Normal ECs) or

colorectal cancer (Tumor ECs) from two different patients. Two endothelial specific markers, vWF and PEM6 showed robust amplification only in the endothelial fractions whereas the ubiquitous housekeeping enzyme GAPDH was observed in all samples. TEM1 (BSC-TEM1), TEM 17 (BSC-TEM7) and TEM22 (BSC-TEM9) were specifically expressed in tumor compared to normal ECs. The cDNA template was diluted 1:10, 1:100, 1:1000, and 1:10,000 as indicated by the declining wedge. (Fig. 4 B- 4J) The endothelial origin of TEMs identified by SAGE was confirmed using *in situ* hybridization as in Fig 3. Expression of TEM 1 (BSC-TEM1) (Fig. 4 B) and TEM17 (BSC-TEM7) (Fig. 4 C) was demonstrated to be highly specific to the ECs in colorectal cancers; sections were imaged in the absence of a counterstain to show the complete lack of detectable expression in the non-endothelial cells of the tumor. Expression of TEM17 (BSC-TEM7) in ECs was demonstrated in a metastatic liver lesion from a primary colorectal cancer (Fig. 4 D), a lung (Fig. 4 E), breast (Fig. 4 F), pancreatic (Fig. 4 G) and brain cancer (Fig. 4 H), as well as in a sarcoma (Fig. 4 I). TEM 17 (BSC-TEM7) was also localized to vessels during normal physiological angiogenesis of the corpus luteum (Fig. 4 J).

DETAILED DESCRIPTION OF THE INVENTION

[51] We identified 46 human genes that were expressed at significantly higher levels (> 10-fold) in tumor endothelium than in normal endothelium, and 33 genes that were expressed at significantly lower levels in human tumor versus normal endothelium. See Tables 2 and 4, respectively. Most of these genes were either not expressed or expressed at relatively low levels in Endothelial Cells (ECs) maintained in culture. Moreover, we identified 93 genes which are expressed in both normal and tumor human endothelium. Interestingly, the tumor endothelium genes were expressed in all tumors tested, regardless of its tissue or organ source. Most tumor endothelium genes were also expressed in corpus luteum and wounds.

[52] As the work has progressed, we have refined and classified our original 46 tumor endothelial markers. We have named these markers TEMs and renumbered them consecutively by the prevalence of their tags in our SAGE analysis. Originally we had not used a consecutive numbering system. Our non-consecutive numbering system has been renamed as BSC-TEMs. For most of the original 46 SAGE Tags, we now provide full-length nucleic acid and protein sequence. In some cases, the sequences were obtained through the public databases, in others the sequences were obtained by cloning and through the use of gene prediction tools. In some cases, we found SAGE Tags corresponding to genes having different splice variants or with known polymorphisms. For example, in one case the SAGE Tag BSC-TEM3 has been found to hybridize to an alternatively spliced form of the transcript encoding BSC-TEM7. The proteins encoded by the two transcripts are the same; therefore they are cumulatively called TEM7. A highly related sequence was found via homology searches, BSC-TEM7R. This paralog sequence is now called TEM3. See Table 2, which follows, showing tumor endothelial markers by order of prevalence (except for TEM 3). Column 1 indicates the prevalence number. Column 2 indicates the original nomenclature. Column 3 indicates the short tags. Column 4 indicates the long tags. Column 5 indicates the accession number in GenBank. Column 6 indicates the sequence identifiers for the short tag, the long tag, the full nucleic acid, and the protein. Column 7 provides a functional description, which is expanded below in the text.

TEM1	BSC- TEM1	GGGGCTGCC CA	GGGGCTGCC GA	NM020404	SEQ ID NO : 94, 309, 195, 196	Human tumor endothelial marker 1 precursor
TEM 2	BSC- TEM2	GATCTCCGT GT			SEQ ID NO: 95, 197.198	sapiens tumor endothelial marker 2 (BSC-TEM2) mRNA/mouse Ras, dexamethasone-induced 1 (RASD1), mRNA
TEM 3	BSC- TEM7 R				SEQ ID NO:199, 200	Human ortholog of mouse paralog of mouse TEM-7
TEM 4		CTTCTTTGA G	CTTCTTTGAGTTT AA	AB034203	SEQ ID NO:97, 311, 201, 202	Homo sapiens dickkopf-3 (DKK-3) mRNA,
TEM 5	BSC- TEM4	TATTAACTCT C	TATTAACTCTCTTTG GA		SEQ ID NO:98, 312, 203, 204	Tumor endothelial marker 4
TEM 6		CAGGAGACC CC	CAGGAGACCCAGG CCC	X57766	SEQ ID NO:99, 314, 205, 206	Human stromelysin-3 mRNA.
TEM 7		GGAAATGTC AA	GGAAATGTCAGCAA GTA	BC002576	SEQ ID NO:100, 315.207, 208	matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase)

TEM 8	CCTGGTTCA GT		SEQ ID NO:101, 316, 209, 210	HeyL transcription factor
TEM 9	BSC- TEM5	TTTTAAGAA C	SEQ ID NO:102, 317, 211, 212	Human collagen alpha-2 type I mRNA, complete cds, clone pHCOL2A1.
TEM 10		TTTGGTTTC C	J03464, M18057, X02488	SEQ ID NO:103, 319, 213, 214
TEM 11		ATTTGTATG A	NM_00250 8	nidogen/entactin
TEM 12		ACTTTAGATG G	X52022	SEQ ID NO:104, 321, 215, 216
TEM 13		GAGTGAGAC CC	M11749	SEQ ID NO:105, 322, 217, 218
TEM 14		GTACACACA CC		H.sapiens RNA for type VI collagen alpha3 chain.
				Human Thy-1 glycoprotein gene, complete cds.
				SEQ ID NO:106, 324, 219, 220
				SEQ ID NO:107, 325, 221, 223
				Cystatin SN

TEM 14	GTACACACA CC	GTACACACACCCCCC ACC	X54867	SEQ ID NO:107, 325, 222, 224	H.sapiens mRNA for cystatin S.
TEM 15	CCACAGGGG AT	CCACAGGGGATTCT CCT	NM_000090	SEQ ID NO:108, 327, 225, 226	Human mRNA 3' region for pro-alpha1(III) collagen.
TEM BSC- 16 TEM6	TAAAGTCA C	TTAAAAGTCACTGTG CA		SEQ ID NO:109, 328, 227, 228	
TEM BSC- 17 TEM7	ACAGACTGTT A	ACAGACTGTTAGGCC AAG	AF279144	SEQ ID NO:110, 329, 229, 230	Human Tumor endothelial marker 7
TEM 18	CCACTGCAC CC			SEQ ID NO:111	
TEM BSC- 19 TEM8	CTATAGGAG AC			SEQ ID NO:112, 330, 231, 232	
TEM 20	GTTCCACAG AA		NM_000089	SEQ ID NO:113, 233, 234	collagen, type I, alpha 2 (COL1A2)

TEM 21	TACCAACCTC CC	TACCACCTCCC CT		SEQ ID NO:114, 331, 235, 236	Homo sapiens mRNA; cDNA DKFZp762B245; (from clone DKFZp762B245);
TEM 22	BSC- TEM9	GCCCTTCTCT T	GCCCCCTTCTCTGTA GTT	NM_00603 9	SEQ ID NO:115, 334, 237, 238
TEM 23		TTAAATAGCA C	TTAAATAGCACCTT AG		endocytic receptor (macrophage mannose receptor family) (KIAA0709),
TEM 24		AGACATACT GA	AGACATACTGACAG AAT	NM_02264 8	SEQ ID NO:116, 335
TEM 25		TCCCCCAGG AG	TCCCCCAGGAGGCCA CCG	NM_00612 9	SEQ ID NO:117, 336, 239, 240
TEM 26				NM_35279, NM_00612 9	SEQ ID NO:118, 338, 241, 242
TEM 27					SEQ ID NO:119
TEM 28				NM_00306 2	No Match
					Homo sapiens mRNA for MEGF5, partial cds.
					Homo sapiens mRNA for KIAA0672 protein, complete cds.

				SEQ ID NO:122, 247, 248	EST's (2 unigene clusters)
TEM 29	TTGGGTGAA AA				
TEM 30	CATTATCCAA A	CATTATCCAA AT	THC53402 9, X68742, AI262158, AI88747, AI394565, AA679721	SEQ ID NO:123, 340, 249, 250	integrin, alpha 1
TEM 31	AGAAACCAC GG	AGAAACCACGGAAA TGG	NM_00184 5	SEQ ID NO:124, 341, 251, 252	hypothetical protein KIAA1164
TEM 32	ACCAAAAC AC			SEQ ID NO:125	no match
TEM 33	TGAAATAAAC		NM_00025 5	SEQ ID NO:126, 253, 254	methylmalonyl Coenzyme A mutase
TEM 34	TTGGTTTCC			SEQ ID NO:127	no match
TEM 35	GTGGAGACCG GA	GTGGAGACCGACTC TGT	ESTAI186 535	SEQ ID NO:128, 345, 255, 358	est

TEM 36	TTTGTGTTGTA A	TTTGTGTTGATATT TA	NM_00437 0	SEQ ID NO:129, 346, 256, 257	est
TEM 37	TTATGTTAA T	TTATGTTAAATAGTT GA	NM_00234 5	SEQ ID NO:130, 347, 258, 259	Human lumican mRNA, complete cds.
TEM 38	TGGAAATGAA C	TGGAAATGACCCAA AAA	NM_00008 8	SEQ ID NO:131, 348, 260, 261	collagen type1 alpha1
TEM 39	TGCCACACACA GT	TGCCACACACAGTGAC TTG	NM_00323 9	SEQ ID NO:132, 350, 262, 263	Human transforming growth factor-beta 3 (TGF- beta3) mRNA, complete
TEM 40	GATGAGGAG AC	GATGAGGAGACTGG CAA		SEQ ID NO:133, 351, 264, 265	collagen, type I, alpha 2
TEM 41	ATCAAAGTT T	ATCAAAGTTATCA TA		SEQ ID NO:134, 352, 266, 267	est
TEM 42	AGTCACATAGTACAT AA		NM_02522 6	SEQ ID NO: 135, 353, 268, 269	ESTs

ITEM 43	TTCGGTTGG TC	TTCGGTTGGTCAA GAT		SEQ ID NO:136, 354	No match
ITEM 44	CCCCACACGG GG	CCCCACACGGCAA GCA	NM_01835 4v	SEQ ID NO: 137, 355, 270, 271	Homo sapiens cDNA FLJ11190 fts, clone PLACE1007583.
ITEM 45	GGCTTGCCT TT	GGCTTGCCTTTGT AT	NM_00036 6	SEQ ID NO:138, 356, 272, 273	est
ITEM 46	ATCCCTTCCC G	ATCCCTTCCC CAC	NM_00268 8	SEQ ID NO:139, 357, 274, 275	Homo sapiens mRNA for peanut-like protein 1, PNUTL1 (hCDCrel-1).

[53] The studies described below provide the first definitive molecular characterization of ECs in an unbiased and general manner. They lead to several important conclusions that have direct bearing on long-standing hypotheses about angiogenesis. First, it is clear that normal and tumor endothelium are highly related, sharing many endothelial cell specific markers. Second, it is equally clear that the endothelium derived from tumors is qualitatively different from that derived from normal tissues of the same type and is also different from primary endothelial cultures. Third, these genes are characteristically expressed in tumors derived from several different tissue types, documenting that tumor endothelium, in general, is different from normal endothelium. Fourth, the genes expressed differentially in tumor endothelium are also expressed during other angiogenic processes such as corpus luteum formation and wound healing. It is therefore more appropriate to regard the formation of new vessels in tumors as "neoangiogenesis" rather than "tumor angiogenesis" *per se*. This distinction is important from a variety of perspectives, and is consistent with the idea that tumors recruit vasculature using much of, or basically the same signals elaborated during other physiologic or pathological processes. That tumors represent "unhealed wounds" is one of the oldest ideas in cancer biology.

[54] The nature and precise biological function of many of the Tumor Endothelial Markers (TEMs) identified here are unknown. Of the previously characterized genes shown in Table 2, it is intriguing that several encode proteins involved in extracellular matrix formation or remodelling (TEM 6, TEM 6, TEM 10, TEM 7, TEM 11, TEM 12, TEM 14, TEM 20, TEM 24, TEM 25, TEM 27, TEM 37, TEM 38, and TEM 40,) Deposition of extracellular matrix is likely critical to the growth of new vessels. Finally, it is perhaps not surprising that so many of the endothelial-specific transcripts identified here, whether expressed only in neovasculature or in endothelium in general, have not been previously characterized, and some are not even represented in EST databases. In part, this may be due to the fact that the EST databases are heavily biased toward certain

tissues, but moreover, may be due to the fact that even in highly vascularized tissues endothelial cells are still a relatively small proportion of the population. Thus, the sensitivity of the SAGE method is a particularly appropriate tool.

- [55] Sequence and literature study has permitted the following identifications to be made among the family of TEM proteins. TEM proteins have been identified which contain transmembrane regions. These include TEM 1, TEM 3, TEM 9, TEM 13, TEM 17, TEM 19, TEM 22, TEM 30, and TEM 44. TEM proteins have been identified which are secreted proteins, including TEM 4, TEM 6, TEM 7, TEM 10, TEM 12, TEM 14, TEM 20, TEM 25, TEM 27, TEM 31, TEM 36, TEM 37, TEM 38, and TEM 39. HeyL (TEM 8) is a transcription factor which may be involved in regulating TEMs as one or more groups. The protein corresponding to the tag for TEM44 was found in the public databases, but no biological function has yet been ascribed to it.
- [56] TEM 1 has been named endosialin in the literature. It has a signal sequence at amino acids 1-17 and a transmembrane domain at amino acids 686-708. Thus it is a cell surface protein. Its extracellular domain is at residues 1-685. Endosialin may be involved in endocytosis. The mouse ortholog is predicted to have a signal peptide at residues 1-21.
- [57] TEM 2 is a dexamethasone induced, ras related protein homolog of 266 amino acids. It has neither a signal sequence nor a transmembrane domain. Thus it is neither a cell surface nor a secreted protein. TEM 2 plays a role in signal transduction. It regulates alterations in cell morphology, proliferation, and cell-extracellular matrix interactions.
- [58] TEM 3 (originally termed TEM 7R) has both a signal sequence (at residues 1-24 or 1-30) and a transmembrane domain (at residues 456 – 477). Thus it is a cell surface protein. The portion of the protein which is extracellular is at amino acids 1- 455. TEM 3 has domains with homology to integrins, plexin,

and adhesion molecules. TEM 3 may regulate GTPases that control signal transduction pathways linking plasma membrane receptors to the actin cytoskeleton. In the mouse ortholog, the signal peptide is predicted to be residues 1-30.

[59] TEM 4 is also known as DKK -3. It has a signal sequence (residues 1-16), suggesting that it is a secreted protein. TEM 4 regulates *wnt* signaling, and it may be involved in vasculogenesis and *wnt*-dependent signaling for endothelial growth. TEM 4 is an inhibitor of Wnt oncogene and such inhibition can be determined by assay. Tsuji et al., Biochem.Biophys.Res.Comm. 268:20-4, 2000.

[60] TEM 5 appears to be neither secreted nor a cell surface protein. TEM 5 appears to be a component of a G protein - GTPase signaling pathway.

[61] TEM 6 is also known as stromelysin - 3 /Matrix metalloproteinase 11 (MMP -11). It has a signal sequence at residues 1-31, but no transmembrane domain. It has an alternative signal peptide splice site at residues 108-109. Thus it appears to be a secreted protein. TEM 6 belongs to the zinc metaloprotease family, also known as the matrixin subfamily. TEM 6 is expressed in most invasive carcinomas. Alpha 1 - protease inhibitor is a natural substrate of MMP 11. TEM 6 degrades extracellular matrix proteins such as collagen and is involved in extracellular matrix remodeling and cell migration. Stromelysin can be assayed using a casein-resorufin substrate, for example. See Tortorella and Arner, Inflammation Research 46 Supp. 2:S122-3, 1997.

[62] TEM 7 is a protein of many names, also being known as matrix metalloproteinase 2, gelatinase A, and 72KD type IV collagenase. TEM 7 has a signal sequence at residues 1-26 and is a secreted protein. Like TEM 6, TEM 7 belongs to the matrixin subfamily (zinc metalloproteinases). TEM 7 cleaves gelatin type I, collagen type I, IV, V VII and X.. TEM 7 associates with integrin on the surface of endothelial cells and promotes vascular invasion. TEM 7 is

involved in tissue remodeling. TEM 7 can be assayed using zymography or quenched fluorescent substrate hydrolysis, for example. Garbett, et al., Molecular Pathology 53:99-106, 2000. A fluorogenic matrix metalloproteinase substrae assay can also be used which employs methoxycoumarin continuaing septapeptide analog of the alpha2(I) collagen cleavage site. See Bhide et al., J. Periodontology 71:690-700, 2000.

[63] TEM 8 is HEYL protein . It has neither a signal sequence nor a transmembrane domain. It is related to the hairy/Enhancer of split genes. TEM 8 is likely a nuclear protein, having a role as a transcription factor. TEM 8 belongs to a new class of Notch signal tranducers and plays a key role in various developmental processes, such as vascular development, somatogenesis and neurogenesis. SNP's at residues 615 and 2201 have Cytosine bases. Notch 3 mutations underlie the CADASIL vascular disorder. See *Mech Dev* 2000 Nov; 98 (1-2):175

[64] TEM 9 is a G- protein coupled receptor homolog, having both a signal sequence at residues 1-26 and 7 transmembrane domains. Thus it is a cell surface protein. Its extracellular region resides in amino acids 1-769. Its transmembrane domains are at residues 817-829 (TM2 and TM3), residues 899-929 (TM4 and TM5), and residues 1034-1040 (TM6 and TM7). TEM 9 acts as a G-protein coupled receptor with extracellular domains characteristic of cell adhesion proteins. One of its splice variants may function as a soluble receptor. TEM 9 may regulate cell polarity and cell migration. It may be involved in exocytosis based on latrophilin function. The mouse ortholog has a predicted signal peptide at residues 1-29.

[65] TEM 10 is collagen type I, alpha2 (COL1A2), which has a signal sequence at residues 1-22. It is an extracellular matrix (ECM) protein which is secreted subsequent to synthesis. TEM 10 interacts with a number of proteins including other ECM proteins, certain growth factors, and matrix metalloproteases. TEM

10 is required for the induction of endothelial tube formation and is involved in tissue remodeling. A variant at nucleotide 3233 which substitutes an A, is associated with osteogenesis imperfecta type IV. A variant at nucleotide 4321 substituting an A retains a wild type phenotype. Nucleotide 715 is a site of a polymorphism. Nucleotides 695-748 are deleted in Ehlers-Danos syndrome. Other mutations are associated with idiopathic osteoporosis, and atypical Marfan syndrome. Variants are known at nucleotides 226(T,C), 314(A,C), 385(T,C), 868 (G,A), 907(C,T), 965(A,G), 970(T,A), 1784 (G,C), 2017(T,G), 2172(C,A), 2284(T,C), 2308(T,C), 2323(T,G), 2344(T,G), 2604(G,A), 2974(A,T), 2903(A,G), 2995(C,T), 3274(C,T), 3581(A,C), 3991(A,C), 4201(G,T), 4434(C,T), 4551(A,C), 4606(C,A), 4947(T,C), 4978(C,T), 4982(G,T), 5051(G,T). PolyA sites are located at nucleotides 4450, 4550, 4885, and 5082. PolyA signals are located at 4420-4424, 4515-4520, 4529-4534, 4866-4871, 5032-5037, 5053-5058. TEM 10, 20, and 40 derive from the same gene but are different isoforms having different lengths.

[66] TEM 11 is Nidogen /Entactin. It is a secreted protein which has a signal sequence at residues 1-28. TEM 11 is an extracellular matrix protein which is a component of a basement membrane. TEM 11 binds to laminin and collagen IV and other extracellular matrix proteins. TEM 11 regulates capillary formation and is involved in tissue remodelling. Variations have been observed at nucleotides 4265(T,C), 4267(G,C,T), and 4738(T,G). Nidogen can be assayed by its effect on the morphology of astrocytes. See Grimpe et al., GLIA 28:138-49, 1999.

[67] TEM 12 is the alpha 3 chain of collagen type VI. It has a signal sequence at residues 1-25. A secreted protein, TEM 12 is an extracellular matrix protein. TEM 12 has a splice variant. TEM 12 is a major constituent of vascular subendothelium and is involved in tissue remodeling. It regulates platelet activation and aggregation. Alternatively spliced domains are located at nucleotides 347-964, 965-1567, 2153-3752, and 4541-5041.

[68] TEM 13 is also known as Thy -1 glycoprotein. It has both a signal sequence (at residues 1-19) and a transmembrane domain (at residues 143-159). Residues 131-161 are removed in a matured form of the protein. The extracellular region of the protein is residues 1- 142 or residues 1-130. TEM 13 has a glycosyl phosphatidylinositol (GPI) anchor at residue 130 anchoring it to the membrane. TEM 13 is detectable in its soluble form in human serum. TEM 13 is reported to be a marker for activated endothelial cells (a marker of adult but not embryonic angiogenesis). TEM 13 on vascular endothelial cells may function as a possible vascular permeability modulator. Antibody to Thy-1 is a mitogenic signal for the CD4+CD45+ and CD8+CD45+ cells, but fails to induce proliferation in the CD45- T cells. Pingel et al., International Immunology 6:169-78, 1994. Thy-1 can be assayed as an inhibitor of such signal.

[69] TEM 14 is also known as cystatin S. It is a secreted protein with a signal sequence at residues 1-20 and an extracellular region at residues 1-141. It is a cysteine protease inhibitor. TEM 14 may regulate cysteine protease function involved in angiogenesis and tissue remodeling. TEM14 is an inhibitor of the activity of papain and such inhibition can be assayed. Hiltke et al., J. Dental Research 78:1401-9, 1999.

[70] TEM 15 is collagen type III, alpha 1 (COL3A1). It has a signal sequence (residues 1-23) and is secreted. Type III collagen binds to von Willebrand factor. It is involved in cell-cell adhesion, proliferation, and migration activities. Variants at nucleotides 2104(C,A), 2194(G,A), 2346(C,T), 2740(C,T), 3157(T), 3468(G), 3652(T), 3666(C), 3693(C), 3755(G), 3756(T), 3824(C), 4546(A, G), 4661(G), 4591(C,T), 4665(C), 5292(C), 5293(C), and 5451 (A) have been observed.

[71] TEM 16 is a tensin homolog which is apparently an intracellular protein. It may have splice variants or isoforms. One form with 1704 amino acids has a region at the N-terminal domain which is similar to a tumor suppressor protein,

phosphatase and tensin homolog (PTEN). Tensin is a focal adhesion molecule that binds to actins and phosphorylated proteins. It is involved in cell migration linking signal transduction pathways to the cytoskeleton. PTEN regulates tumor induced angiogenesis.

[72] TEM 17 (BSC-TEM 7) has a signal sequence which includes residues 1-18 and a transmembrane domain at residues 427-445. It is a cell surface marker with an extracellular region comprising residues 1-426. It has homologs in both mouse and *C. elegans*. Residues 137-244 share weak homology with nidogen; residues 280-344 share homology to PSI domains found in plexin, semaphorins and integrin beta subunits. Variants have been observed at nucleotides 1893(A,G), 1950(C,G), 2042(A,G), and 2220(G,A). In mouse TEM 17 the signal sequence includes residues 1-19.

[73] TEM 19 was originally reported to be tumor endothelial marker 8, i.e., BSC-TEM 8. It has a signal sequence at residues 1-27 and a transmembrane domain at residues 322-343. It is a cell surface protein having an extracellular region at residues 1-321. TEM 19 has a von Willebrand Factor (vWF) A domain at residues 44-216; a domain at residues 34-253 which is found in leukointegrin alpha D chain; and a domain at residues 408-560 found in PRAM-1 or adaptor molecule -1 of the vinculin family. TEM 19's function is adhesion related. von Willibrand Factor domains are typically involved in a variety of functions including vascular processes. TEM 19 may play a role in the migration of vascular endothelial cells. The mouse ortholog has a predicted signal peptide at residues 1-27.

[74] TEM 20 is collagen type I, alpha 2 (COL1A2). It has a signal sequence at residues 1-22 and is a secreted extracellular matrix protein. TEM 20 induces endothelial tube formation *in vitro* and is involved in tissue remodeling. Variants have been observed at nucleotides 226(T,C), 314(A,C), 385(T,C), 868 (G,A), 907(C,T), 965(A,G), 970(T,A), 1784(G,C), 2017(T,G), 2172(C,A), 2284(T,C),

2308(T,C), 2323(T,G), 2344(T,G), 2604(G,A), 2794(A,T), 2903(A,G), 2995(C,T), 3274(C,T), 3581(A,C), 3991(A,C), 4201(G,T), 4434(C,T), 4551(A,C), 4606(C,A), 4895-4901(--, GGACAAAC), 4947(T,C), 4978(C,T), 4982(G,T), 5051(G,T).

[75] TEM 21 is a Formin - like protein homolog which is an intracellular protein. Formin related proteins interact with Rho family small GTPases, profilin, and other actin associated proteins. Formin-binding proteins bind to FH1 domains with their WW domains. TEM 21 has a proline rich FH1 domain at residues 221-449. Formin related proteins play crucial roles in morphogenesis, cell polarity , cytokinesis and reorganization of the actin cytoskeleton. They may also regulate apoptosis, cell adhesion and migration.

[76] TEM 22 is an endocytic receptor in the macrophage mannose receptor family. It has both a signal sequence at residues 1-30 and a transmembrane domain at residues 1415-1435, and resides on the cell surface. Its extracellular domain is amino acids 1- 1414. TEM 22 may be present as a soluble (secreted) form and act as an inhibitor. It may bind secreted phospholipase A2 (sPLA2) and mediate biological responses elicited by sPLA2. TEM 22 may have endocytic properties for sPLA2 and mediate endocytosis for endothelial related proteins. It may promote cell adhesion and be involved in cell-cell communication. Variations have been observed at nucleotide 5389 (A, G). TEM 22 mediates uptake of micro-organisms and host-derived glycoproteins. Groger et al., J. Immunology 165:5428-34, 2000.

[77] TEM 24 is tensin, an intracellular protein. It is a focal adhesion molecule that binds to actin filaments and interacts with phosphotyrosine containing proteins. It may mediate kinase signaling activities and regulate cellular transformation. Variations have been observed at nucleotides 2502 (A, G), 2622(A, G), 6027(A, G). TEM24 binds to actin filaments and interacts with phosphotyrosine-containing proteins. Chen et al., Biochem. J. 351 Pt2:403-11,

2000. TEM24 also binds to phosphoinositide3-kinase. Auger et al., J. Bio. Chem. 271:23452-7, 1996 TEM 24 also binds to nuclear protein p130. Lo et al., Bioessays 16:817-23, 1994.

[78] TEM 25 is Bone morphogenic protein 1 (BMP-1) which has a signal sequence at residues 1-22. It is a secreted protein. There are at least 6 isoforms of BMP-1 as well as splice variants which add carboxy terminal CUB domains and an additional EGF domain. TEM 25 is a metalloprotease enzyme. It cleaves the C-terminal propeptide of collagen type I, II and III and laminin 5 gamma 2 , proteins that are important for vascular processes. It is involved in cartilage formation. Variations have been observed at nucleotides 3106(C,T), 3248(G,A), 3369(G,A). TEM 25 cleave probiglycan at a single site, removing the propeptide and producing a biglycan molecule with an NH(2) terminus identical to that of the mature form found in tissues. Sctt et al., J. Biol. Chem. 275:30504-11, 2000. Laminin alpha 3 and gamma2 short chains are substrates of TEM 25. Amano et al., J. Biol. Chem. 275:22728-35, 2000.

[79] TEM 27 is known as Slit homolog 3, a secreted protein with a signal sequence at residues 1-27. TEM 27 is a secreted guide protein involved in migration, repulsion and patterning. It interacts with "round about" receptors (Robo receptors). TEM 27 may interact with extracellular matrix (ECM) proteins and is involved in cell adhesion. Variations have been observed at nucleotides 4772 (C,T)

[80] TEM 28 is similar to mouse nadrin (neuron specific GTPase activating protein). TEM 28 is an intracellular protein with a RhoGAP domain. The RhoGAP domain activates RhoA, Rac1, and Cdc42 GTPases. It is involved in the reorganization of actin filaments and enhancing exocytosis. It may also be involved in cell signalling. Variations have been observed at nucleotide 3969 (A,C),

[81] TEM 29 is protein tyrosine phosphatase type IVA, member 3, isoform 1, an intracellular protein. It has alternate splice variants. TEM 29 belongs to a small class of prenylated protein tyrosine phosphatases (PTPs). It may be membrane associated by prenylation. PTPs are cell signaling molecules and play regulatory roles in a variety of cellular processes and promote cell proliferation. PTP PRL-3 regulates angiotensin -II induced signaling events.

[82] TEM 30 is integrin alpha 1, a cell surface protein having both a signal sequence (residues 1-28) and a transmembrane domain (residues 1142- 1164). Its extracellular region includes amino acids 1-1141. TEM 30 is a receptor for laminin and collagen. It mediates a variety of adhesive interactions. TEM 30 is abundantly expressed on microvascular endothelial cells. It stimulates endothelial cell proliferation and vascularization. TEM 30 may regulate angiostatin production. Variations have been observed at nucleotide 418 (C,T). TEM 30 activates the Ras/Shc/mitogen-activated protein kinase pathway promoting fibroblast cell proliferation. It also acts to inhibit collagen and metalloproteinase synthesis. Pozzi et al., Proc. Nat. Acad. Sci. USA 97:2202-7, 2000,

[83] TEM 31 is Collagen IV alpha 1 (COL4A1) a secreted protein with a at residues 1-27. TEM 31 is a component of the basement membrane. It binds to alpha3 beta 1 integrin and promotes integrin mediated cell adhesion. Non-collagenous domains of type IV subunits are involved in tumoral angiogenesis. TEM 31 is involved in tissue remodeling. Variations have been observed at nucleotide 4470 (C,T)

[84] TEM 33 is methylmalonyl Co-A Mutase a protein which is localized in the mitochondrial matrix. It degrades several amino acids, odd-numbered-acid fatty acids, and cholesterol to the tricarboxylic acid cycle. A defect in TEM 33 causes a fatal disorder in organic acid metabolism termed methylmalonic aciduria. Variations have been observed at nucleotides 1531(G,A), 1671(G,A), 2028(T,C), 2087(G,A), 2359(A,G), 2437(C,A), 2643(G,C), 2702(G,C). TEM 33

converts L-methylmalonyl CoA to succinyl CoA. This reaction can be assayed as is known in the art. See, e.g., Clin. Chem. 41(8 Pt I):1164-70, 1995.

[85] TEM 36 is collagen type XII, alpha1 (COL12A1), an extracellular matrix protein having a signal sequence at residues 1-23 or 24. TEM 36 has von Willebrand Factor (vWF) type A domains, Fibronectin type III domains, and thrombospondin N-terminal like domain. TEM 36 is expressed in response to stress environment. TEM 36 may organize extracellular matrix architecture and be involved in matrix remodeling. There are two isoforms of the protein, a long form and a short form. The short form is missing amino acids 25-1188, and therefore nucleotides 73 to 3564. Both forms share the signal sequence and are therefore both secreted.

[86] TEM 37 is lumican, an extracellular matrix sulfated proteoglycan having a signal sequence at residues 1-18. Lumican interacts with proteins that are involved in matrix assembly such as collagen type I and type VI; it is involved in cell proliferation and tissue morphogenesis. Lumican plays an important role in the regulation of collagen fiber assembly. Variations have been observed at nucleotides 1021(G,T), 1035(A,G), 1209(A,G), 1259(A,C), 1418(C,A), 1519(T,A). TEM 37 is a binding partner of TGF- β . See FASEB J. 15:559-61, 2000. One assay that can be used to determine TEM 37 activity is a collagen fibril formation/sedimentation assay. Svensson et al., FEBS Letters 470:178-82, 2000.

[87] TEM 38 is collagen type I, alpha 1 (COL1A1), an extracellular matrix protein having a signal sequence at residues 1-22. Type I collagen promotes endothelial cell migration and vascularization and induces tube formation and is involved in tissue remodelling. Telopeptide derivative is used as a marker for malignancy and invasion for certain cancer types. Variations have been observed at nucleotides 296(T,G), 1810(G,A), 1890(G,A), 2204(T,A), 3175(G,C), 3578(C,T), 4298(C,T), 4394(A,T), 4410(A,C), 4415(C.A), 4419 (A,T), 4528(C,A), 4572(G,T), 4602(T,C), 5529(T,C), 5670(C,T), 5985(C,T), 6012(C,T).

[88] TEM 39 is transforming growth factor β -3 (TGF-beta3). It has a signal sequence at residues 1-23. It is a secreted protein. TEM 39 regulates cell growth and differentiation. TGF-beta isoforms play a major role in vascular repair processes and remodeling. Variations have been observed at nucleotide 2020(G,T).

[89] TEM 41 is similar to Olfactomedin like protein. It appears to be an intracellular protein, having no obvious predicted signal sequence. Olfactomedin is the major glycoprotein of the extracellular mucous matrix of olfactory neuroepithelium. TEM 41 shares homology with latrophilin (extracellular regions) which has cell-adhesive type domains. TEM 41 may be involved in adhesive function.

[90] TEM 42 is MSTP032 protein, a cell surface protein having a transmembrane domain at residues 42-61. Its function is unknown and it shares little homology with other proteins. Variations have been observed at nucleotides 418(A,T), 724(C,A).

[91] TEM 44 is a hypothetical protein FLJ11190 (NM_018354) which has two predicted transmembrane domains at residues 121-143 and 176 – 1 97. Residues 144-175 may form an extracellular region. TEM 44's function is not known and shares no homology to other known proteins.

[92] TEM 45 is tropomyosin 1 (alpha), a protein which is intracellular. It forms dimers with a beta subunit. It influences actin function. TEM 45 may be involved in endothelial cell cytoskeletal rearrangement. Variations have been observed at nucleotides 509(A,C), 621(A,C), 635(T,G), 642(C,G), 1059(G,T).

[93] TEM 46 is peanut-like 1 protein/septin 5, which belongs to the septin family. Proteins in the septin family bind to GTP and phosphatidylinositol 4,5-bisphosphate. They are involved in the signal transduction cascades controlling cytokinesis and cell division.

[94] NEM 4 is a member of the small inducible cytokine subfamily A (cys-cys), member 14 (SCYA14). NEM4 is a secreted protein characterized by two adjacent cysteine residues. One isoform lacks internal 16 amino acids compared to isoform 2.

[95] NEM 22 shares homology with guanylate kinase-interacting protein 1Maguin-1. It is a membrane associated protein.

[96] NEM 23 is human signaling lymphocytic acitavation molecule (SLAM). It has a signal sequence at residues 1-20. The extracellular domain may reside at residues 21-237. There is a secreted isoform of the protein.

[97] NEM33 is netrin 4. It induces neurite outgrowth and promotes vascular development. At higher concentration, neurite outgrowth is inhibited.

[98] ECs represent only a minor fraction of the total cells within normal or tumor tissues, and only those EC transcripts expressed at the highest levels would be expected to be represented in libraries constructed from unfractionated tissues. The genes described in the current study should therefore provide a valuable resource for basic and clinical studies of human angiogenesis in the future. Genes which have been identified as tumor endothelial markers (TEMs) correspond to tags shown in SEQ ID NOS: 94-139, 173-176, 180-186. Genes which have been identified as normal endothelial markers (NEMs) correspond to tags shown in SEQ ID NOS: 140-172. Genes which have been identified as pan-endothelial markers (PEMs) *i.e.*, expressed in both tumor and normal endothelial cells correspond to tags shown in SEQ ID NOS: 1-93. Genes which have been previously identified as being expressed predominantly in the endothelium correspond to PEM tags shown in SEQ ID NOS: 1-6, 8, 10-15. Markers in each class can be used interchangeably for some purposes.

[99] Isolated and purified nucleic acids, according to the present invention are those which are not linked to those genes to which they are linked in the human genome. Moreover, they are not present in a mixture such as a library containing a multitude of distinct sequences from distinct genes. They may be, however, linked to other genes such as vector sequences or sequences of other genes to which they are not naturally adjacent. Tags disclosed herein, because of the way that they were made, represent sequences which are 3' of the 3' most restriction enzyme recognition site for the tagging enzyme used to generate the SAGE tags. In this case, the tags are 3' of the most 3' most NlaIII site in the cDNA molecules corresponding to mRNA. Nucleic acids corresponding to tags may be RNA, cDNA, or genomic DNA, for example. Such corresponding nucleic acids can be determined by comparison to sequence databases to determine sequence identities. Sequence comparisons can be done using any available technique, such as BLAST, available from the National Library of Medicine, National Center for Biotechnology Information. Tags can also be used as hybridization probes to libraries of genomic or cDNA to identify the genes from which they derive. Thus, using sequence comparisons or cloning, or combinations of these methods, one skilled in the art can obtain full-length nucleic acid sequences. Genes corresponding to tags will contain the sequence of the tag at the 3' end of the coding sequence or of the 3' untranslated region (UTR), 3' of the 3' most recognition site in the cDNA for the restriction endonuclease which was used to make the tags. The nucleic acids may represent either the sense or the anti-sense strand. Nucleic acids and proteins although disclosed herein with sequence particularity, may be derived from a single individual. Allelic variants which occur in the population of humans are including within the scope of such nucleic acids and proteins. Those of skill in the art are well able to identify allelic variants as being the same gene or protein. Given a nucleic acid, one of ordinary skill in the art can readily determine an open reading frame present, and consequently the sequence of a polypeptide encoded by the open reading frame and, using techniques well known in the art, express such protein in a suitable

host. Proteins comprising such polypeptides can be the naturally occurring proteins, fusion proteins comprising exogenous sequences from other genes from humans or other species, epitope tagged polypeptides, etc. Isolated and purified proteins are not in a cell, and are separated from the normal cellular constituents, such as nucleic acids, lipids, etc. Typically the protein is purified to such an extent that it comprises the predominant species of protein in the composition, such as greater than 50, 60 70, 80, 90, or even 95% of the proteins present.

[100] Using the proteins according to the invention, one of ordinary skill in the art can readily generate antibodies which specifically bind to the proteins. Such antibodies can be monoclonal or polyclonal. They can be chimeric, humanized, or totally human. Any functional fragment or derivative of an antibody can be used including Fab, Fab', Fab2, Fab'2, and single chain variable regions. So long as the fragment or derivative retains specificity of binding for the endothelial marker protein it can be used. Antibodies can be tested for specificity of binding by comparing binding to appropriate antigen to binding to irrelevant antigen or antigen mixture under a given set of conditions. If the antibody binds to the appropriate antigen at least 2, 5, 7, and preferably 10 times more than to irrelevant antigen or antigen mixture then it is considered to be specific.

[101] Techniques for making such partially to fully human antibodies are known in the art and any such techniques can be used. According to one particularly preferred embodiment, fully human antibody sequences are made in a transgenic mouse which has been engineered to express human heavy and light chain antibody genes. Multiple strains of such transgenic mice have been made which can produce different classes of antibodies. B cells from transgenic mice which are producing a desirable antibody can be fused to make hybridoma cell lines for continuous production of the desired antibody. See for example, Nina D. Russel, Jose R. F. Corvalan, Michael L. Gallo, C. Geoffrey Davis, Liise-Anne Pirofski. Production of Protective Human Antipneumococcal Antibodies by Transgenic Mice with Human Immunoglobulin Loci *Infection and Immunity* April 2000, p.

1820-1826; Michael L. Gallo, Vladimir E. Ivanov, Aya Jakobovits, and C. Geoffrey Davis. The human immunoglobulin loci introduced into mice: V (D) and J gene segment usage similar to that of adult humans *European Journal of Immunology* 30: 534-540, 2000; Larry L. Green. Antibody engineering via genetic engineering of the mouse: XenoMouse strains are a vehicle for the facile generation of therapeutic human monoclonal antibodies *Journal of Immunological Methods* 231 11-23, 1999; Yang X-D, Corvalan JRF, Wang P, Roy CM-N and Davis CG. Fully Human Anti-interleukin-8 Monoclonal Antibodies: Potential Therapeutics for the Treatment of Inflammatory Disease States. *Journal of Leukocyte Biology* Vol. 66, pp401-410 (1999); Yang X-D, Jia X-C, Corvalan JRF, Wang P, CG Davis and Jakobovits A. Eradication of Established Tumors by a Fully Human Monoclonal Antibody to the Epidermal Growth Factor Receptor without Concomitant Chemotherapy. *Cancer Research* Vol. 59, Number 6, pp1236-1243 (1999) ; Jakobovits A. Production and selection of antigen-specific fully human monoclonal antibodies from mice engineered with human Ig loci. *Advanced Drug Delivery Reviews* Vol. 31, pp: 33-42 (1998); Green L and Jakobovits A. Regulation of B cell development by variable gene complexity in mice reconstituted with human immunoglobulin yeast artificial chromosomes. *J. Exp. Med.* Vol. 188, Number 3, pp: 483-495 (1998); Jakobovits A. The long-awaited magic bullets: therapeutic human monoclonal antibodies from transgenic mice. *Exp. Opin. Invest. Drugs* Vol. 7(4), pp : 607-614 (1998) ; Tsuda H, Maynard-Currie K, Reid L, Yoshida T, Edamura K, Maeda N, Smithies O, Jakobovits A. Inactivation of Mouse HPRT locus by a 203-bp retrotransposon insertion and a 55-kb gene-targeted deletion: establishment of new HPRT-Deficient mouse embryonic stem cell lines. *Genomics* Vol. 42, pp: 413-421 (1997) ; Sherman-Gold, R. Monoclonal Antibodies: The Evolution from '80s Magic Bullets To Mature, Mainstream Applications as Clinical Therapeutics. *Genetic Engineering News* Vol. 17, Number 14 (August 1997); Mendez M, Green L, Corvalan J, Jia X-C, Maynard-Currie C, Yang X-d, Gallo M, Louie D, Lee D, Erickson K, Luna J, Roy C, Abderrahim H, Kirschenbaum F, Noguchi M,

Smith D, Fukushima A, Hales J, Finer M, Davis C, Zsebo K, Jakobovits A. Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice. *Nature Genetics* Vol. 15, pp: 146-156 (1997); Jakobovits A. Mice engineered with human immunoglobulin YACs: A new technology for production of fully human antibodies for autoimmunity therapy. *Weir's Handbook of Experimental Immunology, The Integrated Immune System* Vol. IV, pp: 194.1-194.7 (1996) ; Jakobovits A. Production of fully human antibodies by transgenic mice. *Current Opinion in Biotechnology* Vol. 6, No. 5, pp: 561-566 (1995) ; Mendez M, Abderrahim H, Noguchi M, David N, Hardy M, Green L, Tsuda H, Yoast S, Maynard-Currie C, Garza D, Gemmill R, Jakobovits A, Klapholz S. Analysis of the structural integrity of YACs comprising human immunoglobulin genes in yeast and in embryonic stem cells. *Genomics* Vol. 26, pp: 294-307 (1995); Jakobovits A. YAC Vectors: Humanizing the mouse genome. *Current Biology* Vol. 4, No. 8, pp: 761-763 (1994); Arbones M, Ord D, Ley K, Ratech H, Maynard-Curry K, Otten G, Capon D, Tedder T. Lymphocyte homing and leukocyte rolling and migration are impaired in L-selectin-deficient mice. *Immunity* Vol. 1, No. 4, pp: 247-260 (1994); Green L, Hardy M, Maynard-Curry K, Tsuda H, Louie D, Mendez M, Abderrahim H, Noguchi M, Smith D, Zeng Y, et. al. Antigen-specific human monoclonal antibodies from mice engineered with human Ig heavy and light chain YACs. *Nature Genetics* Vol. 7, No. 1, pp: 13-21 (1994); Jakobovits A, Moore A, Green L, Vergara G, Maynard-Curry K, Austin H, Klapholz S. Germ-line transmission and expression of a human-derived yeast artificial chromosome. *Nature* Vol. 362, No. 6417, pp: 255-258 (1993) ; Jakobovits A, Vergara G, Kennedy J, Hales J, McGuinness R, Casentini-Borocz D, Brenner D, Otten G. Analysis of homozygous mutant chimeric mice: deletion of the immunoglobulin heavy-chain joining region blocks B-cell development and antibody production. *Proceedings of the National Academy of Sciences USA* Vol. 90, No. 6, pp: 2551-2555 (1993); Kucherlapati et al., U.S. 6,1075,181.

[102] Antibodies can also be made using phage display techniques. Such techniques can be used to isolate an initial antibody or to generate variants with altered specificity or avidity characteristics. Single chain Fv can also be used as is convenient. They can be made from vaccinated transgenic mice, if desired. Antibodies can be produced in cell culture, in phage, or in various animals, including but not limited to cows, rabbits, goats, mice, rats, hamsters, guinea pigs, sheep, dogs, cats, monkeys, chimpanzees, apes.

[103] Antibodies can be labeled with a detectable moiety such as a radioactive atom, a chromophore, a fluorophore, or the like. Such labeled antibodies can be used for diagnostic techniques, either *in vivo*, or in an isolated test sample. Antibodies can also be conjugated, for example, to a pharmaceutical agent, such as chemotherapeutic drug or a toxin. They can be linked to a cytokine, to a ligand, to another antibody. Suitable agents for coupling to antibodies to achieve an anti-tumor effect include cytokines, such as interleukin 2 (IL-2) and Tumor Necrosis Factor (TNF); photosensitizers, for use in photodynamic therapy, including aluminum (III) phthalocyanine tetrasulfonate, hematoporphyrin, and phthalocyanine; radionuclides, such as iodine-131 (¹³¹I), yttrium-90 (⁹⁰Y), bismuth-212 (²¹²Bi), bismuth-213 (²¹³Bi), technetium-99m (^{99m}Tc), rhenium-186 (¹⁸⁶Re), and rhenium-188 (¹⁸⁸Re); antibiotics, such as doxorubicin, adriamycin, daunorubicin, methotrexate, daunomycin, neocarzinostatin, and carboplatin; bacterial, plant, and other toxins, such as diphtheria toxin, pseudomonas exotoxin A, staphylococcal enterotoxin A, abrin-A toxin, ricin A (deglycosylated ricin A and native ricin A), TGF-alpha toxin, cytotoxin from chinese cobra (*naja naja atra*), and gelonin (a plant toxin); ribosome inactivating proteins from plants, bacteria and fungi, such as restrictocin (a ribosome inactivating protein produced by *Aspergillus restrictus*), saporin (a ribosome inactivating protein from *Saponaria officinalis*), and RNase; tyrosine kinase inhibitors; ly207702 (a difluorinated purine nucleoside); liposomes containing antitumor agents (e.g.,

antisense oligonucleotides, plasmids which encode for toxins, methotrexate, etc.); and other antibodies or antibody fragments, such as F(ab).

- [104] Those of skill in the art will readily understand and be able to make such antibody derivatives, as they are well known in the art. The antibodies may be cytotoxic on their own, or they may be used to deliver cytotoxic agents to particular locations in the body. The antibodies can be administered to individuals in need thereof as a form of passive immunization.
- [105] Characterization of extracellular regions for the cell surface and secreted proteins from the protein sequence is based on the prediction of signal sequence, transmembrane domains and functional domains. Antibodies are preferably specifically immunoreactive with membrane associated proteins, particularly to extracellular domains of such proteins or to secreted proteins. Such targets are readily accessible to antibodies, which typically do not have access to the interior of cells or nuclei. However, in some applications, antibodies directed to intracellular proteins may be useful as well. Moreover, for diagnostic purposes, an intracellular protein may be an equally good target since cell lysates may be used rather than a whole cell assay.
- [106] Computer programs can be used to identify extracellular domains of proteins whose sequences are known. Such programs include SMART software (Schultz et al., Proc. Natl. Acad. Sci. USA 95: 5857-5864, 1998) and Pfam software (Bateman et al., Nucleic acids Res. 28: 263-266, 2000) as well as PSORTII. Typically such programs identify transmembrane domains; the extracellular domains are identified as immediately adjacent to the transmembrane domains. Prediction of extracellular regions and the signal cleavage sites are only approximate. It may have a margin of error + or - 5 residues. Signal sequence can be predicted using three different methods (Nielsen et al, *Protein Engineering* 10: 1-6 ,1997, Jagla et. al, *Bioinformatics* 16: 245-250 , 2000, Nakai, K and Horton, P. *Trends in Biochem. Sci.* 24:34-35, 1999) for greater accuracy.

Similarly transmembrane (TM) domains can be identified by multiple prediction methods. (Pasquier, et. al, Protein Eng. 12:381-385, 1999, Sonnhammer et al., In Proc. of Sixth Int. Conf. on Intelligent Systems for Molecular Biology, p. 175-182 , Ed J. Glasgow, T. Littlejohn, F. Major, R. Lathrop, D. Sankoff, and C. Sensen Menlo Park, CA: AAAI Press, 1998 , Klein, et.al, Biochim. Biophys. Acta, 815:468, 1985, Nakai and Kanehisa Genomics, 14: 897-911 , 1992). In ambiguous cases, locations of functional domains in well characterized proteins are used as a guide to assign a cellular localization.

[107] Putative functions or functional domains of novel proteins can be inferred from homologous regions in the database identified by BLAST searches (Altschul et. al. Nucleic Acid Res. 25: 3389-3402, 1997) and/or from a conserved domain database such as Pfam (Bateman et.al, Nucleic Acids Res. 27:260-262 1999) BLOCKS (Henikoff, et. al, Nucl. Acids Res. 28:228-230, 2000) and SMART (Ponting, et. al, Nucleic Acid Res. 27,229-232, 1999). Extracellular domains include regions adjacent to a transmembrane domain in a single transmembrane domain protein (out-in or type I class). For multiple transmembrane domains proteins, the extracellular domain also includes those regions between two adjacent transmembrane domains (in-out and out-in). For type II transmembrane domain proteins, for which the N-terminal region is cytoplasmic, regions following the transmembrane domain is generally extracellular. Secreted proteins on the other hand do not have a transmembrane domain and hence the whole protein is considered as extracellular.

[108] Membrane associated proteins can be engineered to delete the transmembrane domains, thus leaving the extracellular portions which can bind to ligands. Such soluble forms of transmembrane receptor proteins can be used to compete with natural forms for binding to ligand. Thus such soluble forms act as inhibitors. and can be used therapeutically as anti-angiogenic agents, as diagnostic tools for the quantification of natural ligands, and in assays for the identification of small molecules which modulate or mimic the activity of a TEM:ligand complex.

[109] Alternatively, the endothelial markers themselves can be used as vaccines to raise an immune response in the vaccinated animal or human. For such uses, a protein, or immunogenic fragment of such protein, corresponding to the intracellular, extracellular or secreted TEM of interest is administered to a subject. The immunogenic agent may be provided as a purified preparation or in an appropriately expressing cell. The administration may be direct, by the delivery of the immunogenic agent to the subject, or indirect, through the delivery of a nucleic acid encoding the immunogenic agent under conditions resulting in the expression of the immunogenic agent of interest in the subject. The TEM of interest may be delivered in an expressing cell, such as a purified population of tumor endothelial cells or a populations of fused tumor endothelial and dendritic cells. Nucleic acids encoding the TEM of interest may be delivered in a viral or non-viral delivery vector or vehicle. Non-human sequences encoding the human TEM of interest or other mammalian homolog can be used to induce the desired immunologic response in a human subject. For several of the TEMs of the present invention, mouse, rat or other ortholog sequences are described herein or can be obtained from the literature or using techniques well within the skill of the art.

[110] Endothelial cells can be identified using the markers which are disclosed herein as being endothelial cell specific. These include the human markers identified by SEQ ID NOS: 1-172, *i.e.*, the normal, pan-endothelial, and the tumor endothelial markers. Homologous mouse markers include tumor endothelial markers of SEQ ID NO: 182-186 and 190-194. Antibodies specific for such markers can be used to identify such cells, by contacting the antibodies with a population of cells containing some endothelial cells. The presence of cross-reactive material with the antibodies identifies particular cells as endothelial. Similarly, lysates of cells can be tested for the presence of cross-reactive material. Any known format or technique for detecting cross-reactive material can be used including, immunoblots, radioimmunoassay, ELISA, immunoprecipitation, and

immunohistochemistry. In addition, nucleic acid probes for these markers can also be used to identify endothelial cells. Any hybridization technique known in the art including Northern blotting, RT-PCR, microarray hybridization, and *in situ* hybridization can be used.

- [111] One can identify tumor endothelial cells for diagnostic purposes, testing cells suspected of containing one or more TEMs. One can test both tissues and bodily fluids of a subject. For example, one can test a patient's blood for evidence of intracellular and membrane associated TEMs, as well as for secreted TEMs. Intracellular and/or membrane associated TEMs may be present in bodily fluids as the result of high levels of expression of these factors and/or through lysis of cells expressing the TEMs.
- [112] Populations of various types of endothelial cells can also be made using the antibodies to endothelial markers of the invention. The antibodies can be used to purify cell populations according to any technique known in the art, including but not limited to fluorescence activated cell sorting. Such techniques permit the isolation of populations which are at least 50, 60, 70, 80, 90, 92, 94, 95, 96, 97, 98, and even 99 % the type of endothelial cell desired, whether normal, tumor, or pan-endothelial. Antibodies can be used to both positively select and negatively select such populations. Preferably at least 1, 5, 10, 15, 20, or 25 of the appropriate markers are expressed by the endothelial cell population.
- [113] Populations of endothelial cells made as described herein, can be used for screening drugs to identify those suitable for inhibiting the growth of tumors by virtue of inhibiting the growth of the tumor vasculature.
- [114] Populations of endothelial cells made as described herein, can be used for screening candidate drugs to identify those suitable for modulating angiogenesis, such as for inhibiting the growth of tumors by virtue of inhibiting the growth of endothelial cells, such as inhibiting the growth of the tumor or other undesired

vasculature, or alternatively, to promote the growth of endothelial cells and thus stimulate the growth of new or additional large vessel or microvasculature.

[115] Inhibiting the growth of endothelial cells means either regression of vasculature which is already present, or the slowing or the absence of the development of new vascularization in a treated system as compared with a control system. By stimulating the growth of endothelial cells, one can influence development of new (neovascularization) or additional vasculature development (revascularization). A variety of model screen systems are available in which to test the angiogenic and/or anti-angiogenic properties of a given candidate drug. Typical tests involve assays measuring the endothelial cell response, such as proliferation, migration, differentiation and/or intracellular interaction of a given candidate drug. By such tests, one can study the signals and effects of the test stimuli. Some common screens involve measurement of the inhibition of heparanase, endothelial tube formation on Matrigel, scratch induced motility of endothelial cells, platelet-derived growth factor driven proliferation of vascular smooth muscle cells, and the rat aortic ring assay (which provides an advantage of capillary formation rather than just one cell type).

[116] Drugs can be screened for the ability to mimic or modulate, inhibit or stimulate, growth of tumor endothelium cells and/or normal endothelial cells. Drugs can be screened for the ability to inhibit tumor endothelium growth but not normal endothelium growth or survival. Similarly, human cell populations, such as normal endothelium populations or tumor endothelial cell populations, can be contacted with test substances and the expression of tumor endothelial markers and/or normal endothelial markers determined. Test substances which decrease the expression of tumor endothelial markers (TEMs) are candidates for inhibiting angiogenesis and the growth of tumors. Conversely, markers which are only expressed in normal endothelium but not in tumor endothelium (NEMs) can be monitored. Test substances which increase the expression of such NEMs in tumor endothelium and other human cells can be identified as candidate antitumor or

anti-angiogenic drugs. In cases where the activity of a TEM or NEM is known, agents can be screened for their ability to decrease or increase the activity.

- [117] For those tumor endothelial markers identified as containing transmembrane regions, it is desirable to identify drug candidates capable of binding to the TEM receptors found at the cell surface. For some applications, the identification of drug candidates capable of blocking the TEM receptor from its native ligand will be desired. For some applications, the identification of a drug candidate capable of binding to the TEM receptor may be used as a means to deliver a therapeutic or diagnostic agent. For other applications, the identification of drug candidates capable of mimicing the activity of the native ligand will be desired. Thus, by manipulating the binding of a transmembrane TEM receptor:ligand complex, one may be able to promote or inhibit further development of endothelial cells and hence, vascularization.
- [118] For those tumor endothelial markers identified as being secreted proteins, it is desirable to identify drug candidates capable of binding to the secreted TEM protein. For some applications, the identification of drug candidates capable of interfering with the binding of the secreted TEM it is native receptor. For other applications, the identification of drug candidates capable of mimicing the activity of the native receptor will be desired. Thus, by manipulating the binding of the secreted TEM:receptor complex, one may be able to promote or inhibit futher development of endothelial cells, and hence, vascularization.
- [119] Expression can be monitored according to any convenient method. Protein or mRNA can be monitored. Any technique known in the art for monitoring specific genes' expression can be used, including but not limited to ELISAs, SAGE, microarray hybridization, Western blots. Changes in expression of a single marker may be used as a criterion for significant effect as a potential pro-angiogenic, anti-angiogenic or anti-tumor agent. However, it also may be desirable to screen for test substances which are able to modulate the expression

of at least 5, 10, 15, or 20 of the relevant markers, such as the tumor or normal endothelial markers. Inhibition of TEM protein activity can also be used as a drug screen. Human and mouse TEMS can be used for this purpose.

[120] Test substances for screening can come from any source. They can be libraries of natural products, combinatorial chemical libraries, biological products made by recombinant libraries, etc. The source of the test substances is not critical to the invention. The present invention provides means for screening compounds and compositions which may previously have been overlooked in other screening schemes. Nucleic acids and the corresponding encoded proteins of the markers of the present invention can be used therapeutically in a variety of modes. NEMs, can be used to restrict, diminish, reduce, or inhibit proliferation of tumor or other abnormal or undesirable vasculature. TEMs can be used to stimulate the growth of vasculature, such as for wound healing or to circumvent a blocked vessel. The nucleic acids and encoded proteins can be administered by any means known in the art. Such methods include, using liposomes, nanospheres, viral vectors, non-viral vectors comprising polycations, etc. Suitable viral vectors include adenovirus, retroviruses, and sindbis virus. Administration modes can be any known in the art, including parenteral, intravenous, intramuscular, intraperitoneal, topical, intranasal, intrarectal, intrabronchial, etc.

[121] Specific biological antagonists of TEMs can also be used to therapeutic benefit. For example, antibodies, T cells specific for a TEM, antisense to a TEM, and ribozymes specific for a TEM can be used to restrict, inhibit, reduce, and/or diminish tumor or other abnormal or undesirable vasculature growth. Such antagonists can be administered as is known in the art for these classes of antagonists generally. Anti-angiogenic drugs and agents can be used to inhibit tumor growth, as well as to treat diabetic retinopathy, rheumatoid arthritis, psoriasis, polycystic kidney disease (PKD), and other diseases requiring angiogenesis for their pathologies.

[122] Mouse counterparts to human TEMS can be used in mouse cancer models or in cell lines or *in vitro* to evaluate potential anti-angiogenic or anti-tumor compounds or therapies. Their expression can be monitored as an indication of effect. Mouse TEMs are disclosed in SEQ ID NO: 182-186 and 190-194. Mouse TEMs can be used as antigens for raising antibodies which can be tested in mouse tumor models. Mouse TEMs with transmembrane domains are particularly preferred for this purpose. Mouse TEMs can also be used as vaccines to raise an immunological response in a human to the human ortholog.

[123] The above disclosure generally describes the present invention. All references disclosed herein are expressly incorporated by reference. A more complete understanding can be obtained by reference to the following specific examples which are provided herein for purposes of illustration only, and are not intended to limit the scope of the invention.

EXAMPLE 1

Visualization of vasculature of colorectal cancers

[124] The endothelium of human colorectal cancer was chosen to address the issues of tumor angiogenesis, based on the high incidence, relatively slow growth, and resistance to anti-neoplastic agents of these cancers. While certain less common tumor types, such as glioblastomas, are highly vascularized and are regarded as good targets for anti-angiogenic therapy, the importance of angiogenesis for the growth of human colorectal cancers and other common solid tumor types is less well documented.

[125] We began by staining vessels in colorectal cancers using von Willebrand Factor (vWF) as a marker. In each of 6 colorectal tumors, this examination revealed a high density of vessels throughout the tumor parenchyma (Examples in Fig. 1 A and B). Interestingly, these analyses also substantiated the importance of these

vessels for tumor growth, as endothelium was often surrounded by a perivascular cuff of viable cells, with a ring of necrotic cells evident at the periphery (Example in Fig. 1A). Although these preliminary studies suggested that colon tumors are angiogenesis-dependent, reliable markers that could distinguish vessels in colon cancers from the vessels in normal colon are currently lacking. One way to determine if such markers exist is by analyzing gene expression profiles in endothelium derived from normal and neoplastic tissue.

EXAMPLE 2

Purification of endothelial cells

[126] Global systematic analysis of gene expression in tumor and normal endothelium has been hampered by at least three experimental obstacles. First, endothelium is enmeshed in a complex tissue consisting of vessel wall components, stromal cells, and neoplastic cells, requiring highly selective means of purifying ECs for analysis. Second, techniques for defining global gene expression profiles were not available until recently. And third, only a small fraction of the cells within a tumor are endothelial, mandating the development of methods that are suitable for the analysis of global expression profiles from relatively few cells.

[127] To overcome the first obstacle, we initially attempted to purify ECs from dispersed human colorectal tissue using CD31, an endothelial marker commonly used for this purpose. This resulted in a substantial enrichment of ECs but also resulted in contamination of the preparations by hematopoietic cells, most likely due to expression of CD31 by macrophages. We therefore developed a new method for purifying ECs from human tissues using P1H12, a recently described marker for ECs. Unlike CD31, P1H12 was specifically expressed on the ECs of both colorectal tumors and normal colorectal mucosa. Moreover, immunofluorescence staining of normal and cancerous colon with a panel of known cell surface endothelial markers (e.g. VE-cadherin, CD31 and CD34)

revealed that P1H12 was unique in that it stained all vessels including microvessels (see Fig. 2A and data not shown). In addition to selection with P1H12, it was necessary to optimize the detachment of ECs from their neighbors without destroying their cell surface proteins as well as to employ positive and negative affinity purifications using a cocktail of antibodies (Fig. 2B). The ECs purified from normal colorectal mucosa and colorectal cancers were essentially free of epithelial and hematopoietic cells as judged by RT-PCR (Fig. 2C) and subsequent gene expression analysis (see below).

EXAMPLE 3

Comparison of tumor and normal endothelial cell expression patterns

[128] To overcome the remaining obstacles, a modification of the Serial Analysis of Gene Expression (SAGE) technique was used. SAGE associates individual mRNA transcripts with 14 base pair tags derived from a specific position near their 3' termini. The abundance of each tag provides a quantitative measure of the transcript level present within the mRNA population studied. SAGE is not dependent on pre-existing databases of expressed genes, and therefore provides an unbiased view of gene expression profiles. This feature is particularly important in the analysis of cells that constitute only a small fraction of the tissue under study, as transcripts from these cells are unlikely to be well represented in extant EST databases. We adapted the SAGE protocol so that it could be used on small numbers of purified ECs obtained from the procedure outlined in Fig. 2B. A library of ~100,000 tags from the purified ECs of a colorectal cancer, and a similar library from the ECs of normal colonic mucosa from the same patient were generated. These ~193,000 tags corresponded to over 32,500 unique transcripts. Examination of the expression pattern of hematopoietic, epithelial and endothelial markers confirmed the purity of the preparations (Fig. 2D).

EXAMPLE 4

Markers of normal and tumor endothelium

[129] We next sought to identify Pan Endothelial Markers (PEMs), that is, transcripts that were expressed at significantly higher levels in both normal and tumor associated endothelium compared to other tissues. To identify such PEMs, tags expressed at similar levels in both tumor and normal ECs were compared to ~ 1.8 million tags from a variety of cell lines derived from tumors of non-endothelial origin. This simple comparison identified 93 transcripts that were strikingly EC-specific, i.e. expressed at levels at least 20-fold higher in ECs *in vivo* compared to non-endothelial cells in culture. The 15 tags corresponding to characterized genes which were most highly and specifically expressed in endothelium are shown in Table 1A. Twelve of these 15 most abundant endothelial transcripts had been previously shown to be preferentially expressed in endothelium, while the other 3 genes had not been associated with endothelium in the past (Table 1A). These data sets also revealed many novel PEMs, which became increasingly prevalent as tag expression levels decreased (Table 1B). For many of the transcripts, their endothelial origin was confirmed by SAGE analysis of ~401,000 transcripts derived from primary cultures of human umbilical vein endothelial cells (HUVEC) and human dermal microvascular endothelial cells (HMVEC) (Table 1 A and B). To further validate the expression of these PEMs *in vivo*, we developed a highly sensitive non-radioactive *in situ* hybridization method that allowed the detection of transcripts expressed at relatively low levels in frozen sections of human tissues. Two uncharacterized markers, PEM3 and PEM6, were chosen for this analysis. In each case, highly specific expression was clearly limited to vascular ECs in both normal and neoplastic tissues (Fig. 3 A and B and data not shown). These data also suggest that ECs maintained in culture do not completely recapitulate expression patterns observed *in vivo*. For example, Hevin and several other PEM's were expressed at high levels in both tumor and normal

ECs *in vivo*, but few or no transcripts were detected in cultured HUVEC or HMVEC (Table 1). The source of the Hevin transcripts was confirmed to be endothelium by *in situ* hybridization in normal and malignant colorectal tissue (Fig. 3C).

[130] Many of the markers reported in Table 1 were expressed at significantly higher levels than previously characterized genes commonly associated with ECs. For example, the top 25 markers were all expressed at greater than 200 copies per cell. In contrast, the receptors for VEGF (VEGFR-1 and VEGFR-2) were expressed at less than 20 copies per cell. Interestingly, VEGFR2 (KDR), which had previously been reported to be up-regulated in vessels during colon cancer progression , was found to be expressed in both normal and neoplastic colorectal tissue (Fig. 3 D and E). The lack of specificity of this gene was in accord with the SAGE data, which indicated that the VEGFR was expressed at 12 copies per cell in both normal and tumor endothelium.

EXAMPLE 5

Tumor *versus* normal endothelium

[131] We next attempted to identify transcripts that were differentially expressed in endothelium derived from normal or neoplastic tissues. This comparison revealed 33 tags that were preferentially expressed in normal-derived endothelium at levels at least 10-fold higher than in tumor-derived endothelium. Conversely, 46 tags were expressed at 10-fold or higher levels in tumor vessels. Because those transcripts expressed at higher levels in tumor endothelium are most likely to be useful in the future for diagnostic and therapeutic purposes, our subsequent studies focussed on this class. Of the top 25 tags most differentially expressed, 12 tags corresponded to 11 previously identified genes, one with an alternative polyadenylation site (see Table 2). Of these 10 genes, 6 have been recognized as markers associated with angiogenic vessels. The remaining 14 tags corresponded

to uncharacterised genes, most of which have only been deposited as ESTs (Table 2).

[132] To validate the expression patterns of these genes, we chose to focus on 9 Tumor Endothelial Markers (BSC-TEM 1-9; TEM 1, 2, 5, 9, 16, 17, 19, and 22) for which EST sequences but no other information was available (Table 2). These tags were chosen simply because they were among the most differentially expressed on the list and because we were able to obtain suitable probes. In many cases, this required obtaining near full-length sequences through multiple rounds of sequencing and cDNA walking (See accession numbers in Table 2). RT-PCR analysis was then used to evaluate the expression of the corresponding transcripts in purified ECs derived from normal and tumor tissues of two patients different from the one used to construct the SAGE libraries. As shown in Fig. 4 A, the vWF gene, expected to be expressed in both normal and tumor endothelium on the basis of the SAGE data as well as previous studies, was expressed at similar levels in normal and tumor ECs from both patients, but was not expressed in purified tumor epithelial cells. As expected, PEM2 displayed a pattern similar to vWF. In contrast, all 9 TEMs chosen for this analysis were prominently expressed in tumor ECs, but were absent or barely detectable in normal ECs (Table 3 and examples in Fig. 4A). It is important to note that these RT-PCR assays were extremely sensitive indicators of expression, and the absence of detectable transcripts in the normal endothelium, combined with their presence in tumor endothelial RNAs even when diluted 100-fold, provides compelling confirmatory evidence for their differential expression. These results also show that these transcripts were not simply expressed differentially in the ECs of the original patient, but were characteristic of colorectal cancer endothelium in general.

[133] It could be argued that the results noted above were compromised by the possibility that a small number of non-endothelial cells contaminated the cell populations used for SAGE and RT-PCR analyses, and that these non-endothelial

cells were responsible for the striking differences in expression of the noted transcripts. To exclude this possibility, we performed *in situ* hybridization on normal and neoplastic colon tissue. In every case where transcripts could be detected (BSC-TEM 1, 3, 4, 5, 7, 8, and 9; TEM 1, 5, 9, 17, and 19), they were specifically localized to ECs (Table 3 and examples in Fig. 4 B and C). Although caution must be used when interpreting negative *in situ* hybridization results, none of the TEMs were expressed in vascular ECs associated with normal colorectal tissue even though vWF and Hevin were clearly expressed (Table 3).

EXAMPLE 6

Tumor endothelium markers are expressed in multiple tumor types

[134] Were these transcripts specifically expressed in the endothelium within primary colorectal cancers, or were they characteristic of tumor endothelium in general? To address this question, we studied the expression of a representative TEM (BSC-TEM7; TEM 17) in a liver metastasis from a colorectal cancer, a sarcoma, and in primary cancers of the lung, pancreas, breast and brain. As shown in Fig. 4, the transcript was found to be expressed specifically in the endothelium of each of these cancers, whether metastatic (Fig. 4D) or primary (Fig. 4E-I). Analysis of the other six TEMs, (BSC-TEM 1, 3, 4, 5, 7, 8 and 9; TEM 1, 5, 9, 17, and 19) revealed a similar pattern in lung tumors, brain tumors, and metastatic lesions of the liver (see Table 3).

EXAMPLE 7

Tumor endothelium markers are neo-angiogenic

[135] Finally, we asked whether these transcripts were expressed in angiogenic states other than that associated with tumorigenesis. We thus performed *in situ* hybridizations on corpus luteum tissue as well as healing wounds. Although there

were exceptions, we found that these transcripts were generally expressed both in the corpus luteum and in the granulation tissue of healing wounds (Table 3 and example in Fig. 4J). In all tissues studied, expression of the genes was either absent or exclusively confined to the EC compartment.

References and Notes

The disclosure of each reference cited is expressly incorporated herein.

1. J. Folkman, in *Cancer Medicine* J. Holland, Bast Jr, RC, Morton DL, Frei III, E, Kufe, DW, Weichselbaum, RR, Ed. (Williams & Wilkins, Baltimore, 1997) pp. 181.
2. R. S. Kerbel, *Carcinogenesis* 21, 505 (2000).
3. P. Wesseling, D. J. Ruiter, P. C. Burger, *J Neurooncol* 32, 253 (1997).
4. Q. G. Dong, et al., *Arterioscler Thromb Vasc Biol* 17, 1599 (1997).
5. P. W. Hewett, J. C. Murray, *In Vitro Cell Dev Biol Anim* 32, 462 (1996).
6. M. A. Hull, P. W. Hewett, J. L. Brough, C. J. Hawkey, *Gastroenterology* 111, 1230 (1996).
7. G. Haraldsen, et al., *Gut* 37, 225 (1995).
8. The original EC isolation protocol was the same as that shown in Fig. 2B except that dispersed cells were stained with anti-CD31 antibodies instead of anti-P1H12, and magnetic beads against CD64 and CD14 were not included in the negative selection. After generating 120,000 SAGE tags from these two EC preparations, careful analysis of the SAGE data revealed that, in addition to endothelial-specific markers, several macrophage-specific markers were also present.
9. A. Solovey, et al., *N Engl J Med* 337, 1584 (1997).
10. V. E. Velculescu, L. Zhang, B. Vogelstein, K. W. Kinzler, *Science* 270, 484-487 (1995).
11. In order to reduce the minimum amount of starting material required from ~50 million cells to ~50,000 cells (i.e. ~1000-fold less) we and others (38) have introduced

several modifications to the original SAGE protocol. A detailed version of our modified "MicroSAGE" protocol is available from the authors upon request.

12. 96,694 and 96,588 SAGE tags were analyzed from normal and tumor derived ECs, respectively, and represented 50,298 unique tags. A conservative estimate of 32,703 unique transcripts was derived by considering only those tags observed more than once in the current data set or in the 134,000 transcripts previously identified in human transcriptomes (39).

13. To identify endothelial specific transcripts, we normalized the number of tags analyzed in each group to 100,000, and limited our analysis to transcripts that were expressed at levels at least 20-fold higher in ECs than in non-endothelial cell lines in culture and present at fewer than 5 copies per 100,000 transcripts in non-endothelial cell lines and the hematopoietic fraction (~57,000 tags)(41). Non-endothelial cell lines consisted of 1.8×10^6 tags derived from a total of 14 different cancer cell lines including colon, breast, lung, and pancreatic cancers, as well as one non-transformed keratinocyte cell line, two kidney epithelial cell lines, and normal monocytes. A complete list of PEMs is available at www.sagenet.org\angio\table1.htm.

14. M. Tucci, et al., *J Endocrinol* 157, 13 (1998).
15. T. Oono, et al., *J Invest Dermatol* 100 , 329 (1993).
16. K. Motamed, *Int J Biochem Cell Biol* 31, 1363 (1999).
17. N. Bardin, et al., *Tissue Antigens* 48, 531 (1996).
18. D. M. Bradham, A. Igarashi, R. L. Potter, G. R. Grotendorst, *J Cell Biol* 114, 1285 (1991).
19. K. Akaogi, et al., *Proc Natl Acad Sci U S A* 93, 8384 (1996).

20. Y. Muragaki, et al., *Proc Natl Acad Sci U S A* 92, 8763 (1995).
21. M. L. Iruela-Arispe, C. A. Diglio, E. H. Sage, *Arterioscler Thromb* 11, 805 (1991).
22. J. P. Girard, T. A. Springer, *Immunity* 2, 113 (1995).
23. E. A. Jaffe, et al., *J Immunol* 143, 3961 (1989).
24. J. P. Girard, et al., *Am J Pathol* 155, 2043 (1999).
25. H. Ohtani, N. Sasano, *J Electron Microsc* 36, 204 (1987).
26. For non-radioactive *in situ* hybridization, digoxigenin (DIG)-labelled sense and anti-sense riboprobes were generated through PCR by amplifying 500-600 bp products and incorporating a T7 promoter into the anti-sense primer. In vitro transcription was performed using DIG RNA labelling reagents and T7 RNA polymerase (Roche, Indianapolis, IN). Frozen tissue sections were fixed with 4 % paraformaldehyde, permeabilized with pepsin, and incubated with 200 ng/ml of riboprobe overnight at 55°C. For signal amplification, a horseradish peroxidase (HRP) rabbit anti-DIG antibody (DAKO, Carpinteria, CA) was used to catalyse the deposition of Biotin-Tyramide (from GenPoint kit, DAKO). Further amplification was achieved by adding HRP rabbit anti-biotin (DAKO), biotin-tyramide, and then alkaline-phosphatase (AP) rabbit anti-biotin (DAKO). Signal was detected using the AP substrate Fast Red TR/Naphthol AS-MX (Sigma, St. Louis, MO), and cells were counterstained with hematoxylin unless otherwise indicated. A detailed protocol including the list of primers used to generate the probes can be obtained from the authors upon request.
27. Transcript copies per cell were calculated assuming an average cell contains 300,000 transcripts.

28. R. S. Warren, H. Yuan, M. R. Matli, N. A. Gillett, N. Ferrara, *J Clin Invest* 95, 1789 (1995).
29. Y. Takahashi, Y. Kitadai, C. D. Bucana, K. R. Cleary, L. M. Ellis, *Cancer Res* 55, 3964 (1995).
30. L. F. Brown, et al., *Cancer Res* 53, 4727 (1993).
31. Endothelial-specific transcripts were defined as those expressed at levels at least 5-fold higher in ECs *in vivo* than in non-endothelial cell lines in culture (13), and present at no more than 5 copies per 100,000 transcripts in non-endothelial cell lines and the hematopoietic cell fraction (41). Transcripts showing statistically different levels of expression ($P < 0.05$) were then identified using Monte Carlo analysis as previously described (40). Transcripts preferentially expressed in normal endothelium were then defined as those expressed at levels at least 10-fold higher in normal endothelium than in tumor endothelium. Conversely, tumor endothelial transcripts were at least 10-fold higher in tumor versus normal endothelium. See www.sagenet.org\angio\table2.htm and www.sagenet.org\angio\table3.htm for a complete list of differentially expressed genes.
32. M. Iurlaro, et al., *Eur J Clin Invest* 29 , 793 (1999).
33. W. S. Lee, et al., *Circ Res* 82, 845 (1998).
34. J. Niquet, A. Represa, *Brain Res Dev Brain Res* 95, 227 (1996).
35. L. Fousser, L. Irueala-Arispe, P. Bornstein, E. H. Sage, *J Biol Chem* 266 , 18345 (1991).
36. M. L. Irueala-Arispe, P. Hasselaar, H. Sage, *Lab Invest* 64, 174 (1991).
37. H. F. Dvorak, *N Engl J Med* 315, 1650 (1986).
38. B. Virlon, et al., *Proc Natl Acad Sci U S A* 96, 15286 (1999).

39. V. E. Velculescu, et al., *Nat Genet* 23, 387 (1999).
40. L. Zhang, et al., *Science* 276, 1268 (1997).
41. Human colon tissues were obtained within ½ hour after surgical removal from patients. Sheets of epithelial cells were peeled away from normal tissues with a glass slide following treatment with 5 mM DDT, then 10 mM EDTA, leaving the lamina propria intact. After a 2h incubation in collagenase at 37 oC, cells were filtered sequentially through 400 um, 100 um, 50 um and 25 um mesh, and spun through a 30 % pre-formed Percoll gradient to pellet RBCs. Epithelial cells (Epithelial Fraction), which were found to non-specifically bind magnetic beads, were removed using Dynabeads coupled to BerEP4 (Dynal, Lake Success, NY). Subsequently, macrophages and other leukocytes (Hematopoietic Fraction) were removed using a cocktail of beads coupled to anti-CD45, anti-CD14 and anti-CD64 (Dynal). The remaining cells were stained with P1H12 antibody, purified with anti-mouse IgG-coupled magnetic beads, and lysed in mRNA lysis buffer. A detailed protocol can be obtained from the authors upon request.
42. H. Sheikh, H. Yarwood, A. Ashworth, C. M. Isacke, *J Cell Sci* 113, 1021-32 (2000).

Sequence name	SEQ ID NO:
PEM 1	1
PEM 2	2
PEM 3	3
PEM 4	4
PEM 5	5
PEM 6	6
PEM 7	7
PEM 8	8
PEM 9	9
PEM 10	10
PEM 11	11
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PEM 14	14
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TEM 7 DNA	175
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TEM 2 Protein	178
TEM 8 Protein	179
TEM 5 DNA	180
TEM 7B DNA	181
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mTEM 5 DNA	183
mTEM 7 DNA	184
mTEM 7B DNA	185
mTEM 8 DNA	186
TEM 8 Protein	187
TEM 5 Protein	188
TEM 7B Protein	189
mTEM 1 Protein	190
mTEM 5 Protein	191

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181	TEM 7B DNA
182	mTEM 1 DNA
183	mTEM 5 DNA
184	mTEM 7 DNA
185	mTEM 7B DNA
186	mTEM 8 DNA
187	TEM 8 Protein
188	TEM 5 Protein
189	TEM 7B Protein
190	mTEM 1 Protein
191	mTEM 5 Protein

mTEM 7 Protein	192
mTEM 7b Protein	193
mTEM 8 Protein	194
TEM 1 DNA	195
TEM 1 Protein	196
TEM 2 DNA	197
TEM 2 Protein	198
TEM 3 DNA	199
TEM 3 Protein	200
TEM 4 DNA	201
TEM 4 Protein	202
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TEM 5 Protein	204
TEM 6 DNA	205
TEM 6 Protein	206
TEM 7 DNA	207
TEM 7 Protein	208
TEM 8 DNA	209
TEM 8 Protein	210
TEM 9 DNA	211
TEM 9 Protein	212
TEM 10 DNA	213
TEM 10 Protein	214
TEM 11 DNA	215
TEM 11 Protein	216
TEM 12 DNA	217
TEM 12 Protein	218
TEM 13 DNA	219
TEM 13 Protein	220
TEM 14a DNA	221
TEM 14b DNA	222
TEM 14a Protein	223
TEM 14b Protein	224
TEM 15 DNA	225
TEM 15 Protein	226
TEM 16 DNA	227
TEM 16 Protein	228
TEM 17 DNA	229
TEM 17 Protein	230

192	mTEM 7 Protein
193	mTEM 7b Protein
194	mTEM 8 Protein
195	TEM 1 DNA
196	TEM 1 Protein
197	TEM 2 DNA
198	TEM 2 Protein
199	TEM 3 DNA
200	TEM 3 Protein
201	TEM 4 DNA
202	TEM 4 Protein
203	TEM 5 DNA
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207	TEM 7 DNA
208	TEM 7 Protein
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218	TEM 12 Protein
219	TEM 13 DNA
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222	TEM 14b DNA
223	TEM 14a Protein
224	TEM 14b Protein
225	TEM 15 DNA
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227	TEM 16 DNA
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229	TEM 17 DNA
230	TEM 17 Protein

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TEM 39 Protein	263
TEM 40 DNA	264
TEM 40 Protein	265
TEM 41 DNA	266
TEM 41 Protein	267
TEM 42 DNA	268

231	TEM 19 DNA
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233	TEM 20 DNA
234	TEM 20 Protein
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236	TEM 21 Protein
237	TEM 22 DNA
238	TEM 22 Protein
239	TEM 24 DNA
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262	TEM 39 DNA
263	TEM 39 Protein
264	TEM 40 DNA
265	TEM 40 Protein
266	TEM 41 DNA
267	TEM 41 Protein
268	TEM 42 DNA
269	TEM 42 Protein

TEM 42 Protein	269
TEM 44 DNA	270
TEM 44 Protein	271
TEM 45 DNA	272
TEM 45 Protein	273
TEM 46 DNA	274
TEM 46 Protein	275
NEM 4 DNA	276
NEM 4 Protein	277
NEM 14 DNA	278
NEM 14 Protein	279
NEM 17 DNA	280
NEM 17 Protein	281
NEM 22 DNA	282
NEM 22 Protein	283
NEM 23 DNA	284
NEM 23 Protein	285
NEM 23 Secreted	286
NEM 23 Short	287
NEM 33 DNA	288
NEM 33 Protein	289
mTEM 1 DNA	290
mTEM 1 Protein	291
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mTEM 2 Protein	293
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mTEM 3 Protein	299
mTEM 9 DNA	294
mTEM 9 Protein	295
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mTEM 13 Protein	303
mTEM 17 DNA	296
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mTEM 22 DNA	304
mTEM 22 Protein	305
mTEM 30 DNA	306
mTEM 30 Protein	307

270	TEM 44 DNA
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272	TEM 45 DNA
273	TEM 45 Protein
274	TEM 46 DNA
275	TEM 46 Protein
276	NEM 4 DNA
277	NEM 4 Protein
278	NEM 14 DNA
279	NEM 14 Protein
280	NEM 17 DNA
281	NEM 17 Protein
282	NEM 22 DNA
283	NEM 22 Protein
284	NEM 23 DNA
285	NEM 23 Protein
286	NEM 23 Secreted
287	NEM 23 Short
288	NEM 33 DNA
289	NEM 33 Protein
290	mTEM 1 DNA
291	mTEM 1 Protein
292	mTEM 2 DNA
293	mTEM 2 Protein
294	mTEM 9 DNA
295	mTEM 9 Protein
296	mTEM 17 DNA
297	mTEM 17 Protein
298	mTEM 3 DNA
299	mTEM 3 Protein
300	mTEM 19 DNA
301	mTEM 19 Protein
302	mTEM 13 DNA
303	mTEM 13 Protein
304	mTEM 22 DNA
305	mTEM 22 Protein
306	mTEM 30 DNA
307	mTEM 30 Protein
308	TEM 2 tag

TEM 2 tag	308
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TEM 3 long tag	310
TEM 4 long tag	311
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TEM 5 long tag	313
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TEM 9 long tag	317
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TEM 10 long tag	320
TEM 11 long tag	321
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TEM 36 long tag	346

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347	TEM 37 long tag

TEM 37 long tag	347
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TEM 38 long tag	349
TEM 39 long tag	350
TEM 40 long tag	351
TEM 41 long tag	352
TEM 42 long tag	353
TEM 43 long tag	354
TEM 44 long tag	355
TEM 45 long tag	356
TEM 46 long tag	357

348	TEM 38 long tag
349	TEM 38 long tag
350	TEM 39 long tag
351	TEM 40 long tag
352	TEM 41 long tag
353	TEM 42 long tag
354	TEM 43 long tag
355	TEM 44 long tag
356	TEM 45 long tag
357	TEM 46 long tag
358	TEM 35 Protein

CLAIMS

1. An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 17, 19, and 44, as shown in SEQ ID NO: 196, 212, 230, 232, and 271, respectively.
2. The isolated molecule of claim 1 which is an intact antibody molecule.
3. The isolated molecule of claim 1 which is a single chain variable region (ScFv).
4. The isolated molecule of claim 1 which is a monoclonal antibody.
5. The isolated molecule of claim 1 which is a humanized antibody.
6. The isolated molecule of claim 1 which is a human antibody.
7. The isolated molecule of claim 1 which is bound to a cytotoxic moiety.
8. The isolated molecule of claim 1 which is bound to a therapeutic moiety.
9. The isolated molecule of claim 1 which is bound to a detectable moiety.
10. The isolated molecule of claim 1 which is bound to an anti-tumor agent.

11. A method of inhibiting neoangiogenesis, comprising:
 - administering to a subject in need thereof an effective amount of an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 17, 19, 22, and 44, as shown in SEQ ID NO: 196, 212, 230, 232, 238, and 271, respectively, whereby neoangiogenesis is inhibited.
12. The method of claim 11 wherein the subject bears a vascularized tumor.
13. The method of claim 11 wherein the subject has polycystic kidney disease.
14. The method of claim 11 wherein the subject has diabetic retinopathy.
15. The method of claim 11 wherein the subject has rheumatoid arthritis.
16. The method of claim 11 wherein the subject has psoriasis.

17. A method of inhibiting tumor growth, comprising:

administering to a human subject bearing a tumor an effective amount of an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 17, 19, 22, and 44, as shown in SEQ ID NO: 196, 212, 230, 232, 238, and 271, respectively, whereby growth of the tumor is inhibited.

18. An isolated molecule comprising an antibody variable region

which specifically binds to a TEM protein selected from the group consisting of: 9, 17, 19, and 44, as shown in SEQ ID NO: 212, 230, 232, and 271, respectively.

19. The isolated molecule of claim 18 which is a single chain variable region (ScFv).

20. The isolated molecule of claim 18 which is a monoclonal antibody.

21. The isolated molecule of claim 18 which is a humanized antibody.

22. The isolated molecule of claim 18 which is a human antibody.

23. The isolated molecule of claim 18 which is bound to a cytotoxic moiety.

24. The isolated molecule of claim 18 which is bound to a therapeutic moiety.

25. The isolated molecule of claim 18 which is bound to a detectable

moiety.

26. The isolated molecule of claim 18 which is bound to an anti-tumor agent.
27. The isolated molecule of claim 18 which is an intact antibody molecule.
28. An isolated and purified human transmembrane protein selected from the group consisting of: TEM 9, 17, and 19 as shown in SEQ ID NO: 212, 230, and 232, respectively.
29. An isolated and purified nucleic acid molecule comprising a coding sequence for a transmembrane TEM selected from the group consisting of: TEM 9, 17, and 19 as shown in SEQ ID NO: 212, 230, 232, respectively.
30. The isolated and purified nucleic acid molecule of claim 29 which comprises a coding sequence selected from those shown in SEQ ID NO: 211, 229, and 231.
31. A recombinant host cell which comprises a nucleic acid molecule comprising a coding sequence for a transmembrane TEM selected from the group consisting of: TEM 9, 17, and 19 as shown in SEQ ID NO: 212, 230, and 232, respectively.
32. The recombinant host cell of claim 31 which comprises a coding sequence selected from those shown in SEQ ID NO: 211, 229, and 231.
33. A method of inducing an immune response in a mammal, comprising:
administering to the mammal a nucleic acid molecule comprising a coding sequence for a human transmembrane protein selected from the group consisting of: TEM 1, 9, 13, 17, 19, 22, 30, and 44 as shown in SEQ ID NO: 196, 212, 220, 230, 232, 238, 250 and 271, respectively, whereby an immune response to the human transmembrane protein is induced in the mammal.

34. The method of claim 33 wherein the coding sequence is shown in SEQ ID NO: 195, 211, 219, 229, 231, 237, 249, 270.

35. A method of inducing an immune response in a mammal, comprising:

administering to the mammal a purified human transmembrane protein selected from the group consisting of: TEM 1, 9, 13, 17, 19, 22, 30, and 44 as shown in SEQ ID NO: 196, 212, 220, 230, 232, 238, 250 and 271 , respectively, whereby an immune response to the human transmembrane protein is induced in the mammal.

36. A method for identification of a ligand involved in endothelial cell regulation, comprising:

contacting a test compound with an isolated and purified human transmembrane protein selected from the group consisting of 1, 9, 13, 17, 19, 30, and 44 as shown in SEQ ID NO: 196, 212, 220, 230, 250, 232 and 271;

contacting the isolated and purified human transmembrane protein with a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 13, 17, 19, 30, and 44 as shown in SEQ ID NO: 196, 212, 220, 230, 250, 232 and 271, respectively;

determining binding of the molecule comprising an antibody variable region to the human transmembrane protein, wherein a test compound which diminishes the binding of the molecule comprising an antibody variable region to the human transmembrane protein is identified as a ligand involved in endothelial cell regulation.

37. A method for identification of a ligand involved in endothelial cell regulation, comprising:

contacting a test compound with a cell comprising a human transmembrane protein selected from the group consisting of 1, 9, 17, and 19 as shown in SEQ ID NO: 196, 212, 230, and 232;

contacting the cell with a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 17, and 19 as shown in SEQ ID NO: 196, 212, 230, and 232, respectively;

determining binding of the molecule comprising an antibody variable region to the cell, wherein a test compound which diminishes the binding of the molecule comprising an antibody variable region to the cell is identified as a ligand involved in endothelial cell regulation.

38. A soluble form of a human transmembrane protein selected from

the group consisting of: TEM 1, 9, 17, 19, 22, 30 and 44 as shown in SEQ ID NO: 196, 212, 230, 232, 238, 250, and 271, respectively, wherein the soluble forms lack transmembrane domains.

39. The soluble form of claim 38 wherein the soluble form consists of an extracellular domain of the human transmembrane protein.

40. A method of inhibiting neoangiogenesis in a patient, comprising:
administering to the patient a soluble form of a human

transmembrane protein according to claim 38, whereby neoangiogenesis in the patient is inhibited.

41. A method of inhibiting neoangiogenesis in a patient, comprising:

administering to the patient a soluble form of a human transmembrane protein according to claim 39, whereby neoangiogenesis in the patient is inhibited.

42. The method of claim 40 wherein the patient bears a vascularized tumor.

43. The method of claim 41 wherein the patient bears a vascularized tumor.

44. The method of claim 40 wherein the patient has polycystic kidney disease.
45. The method of claim 40 wherein the patient has diabetic retinopathy.
46. The method of claim 40 wherein the patient has rheumatoid arthritis.
47. The method of claim 40 wherein the patient has psoriasis.
48. The method of claim 41 wherein the patient has polycystic kidney disease.
49. The method of claim 41 wherein the patient has diabetic retinopathy.
50. The method of claim 41 wherein the patient has rheumatoid arthritis.
51. The method of claim 41 wherein the patient has psoriasis.
52. A method of identifying regions of neoangiogenesis in a patient, comprising:
administering to a patient a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 13, 17, 19, 22, 30, and 44, as shown in SEQ ID NO: 196, 212, 220, 230, 232, 238, 250, and 271, respectively, wherein the molecule is bound to a detectable moiety; and
detecting the detectable moiety in the patient, thereby identifying neoangiogenesis.
53. A method of screening for neoangiogenesis in a patient, comprising:

contacting a body fluid collected from the patient with a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 17, 19, and 44, as shown in SEQ ID NO: 196, 212, 230, 232, and 271, respectively, wherein detection of cross-reactive material in the body fluid with the molecule indicates neoangiogenesis in the patient.

54. A method of screening for neoangiogenesis in a patient, comprising:

contacting a body fluid collected from the patient with a molecule comprising an antibody variable region which specifically binds to a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 25, 27, 31, 36, 37, 38, 39, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 242, 244, 252, 257, 259, 261, and 263, respectively, wherein detection of cross-reactive material in the body fluid with the molecule indicates neoangiogenesis in the patient.

55. A method of promoting neoangiogenesis in a patient, comprising:

administering to a patient in need of neoangiogenesis a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 234, 242, 244, 252, 257, 259, 261, 263, and 265, whereby neoangiogenesis in the patient is stimulated.

56. A method of promoting neoangiogenesis in a patient, comprising:

administering to a patient in need of neoangiogenesis a nucleic acid molecule encoding a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 234, 242, 244, 252, 257, 259, 261, 263, and 265, whereby the TEM protein is expressed and neoangiogenesis in the patient is stimulated.

57. A method of screening for neoangiogenesis in a patient, comprising:

detecting a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 234, 242, 244, 252, 257, 259, 261, 263, and 265, respectively, in a body fluid collected from the patient, wherein detection of the TEM protein indicates neoangiogenesis in the patient.

58. A method of screening for neoangiogenesis in a patient, comprising:

detecting in a body fluid collected from the patient a nucleic acid encoding a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, wherein the nucleic acid is selected from the group consisting of those shown in SEQ ID NO: 201, 205, 207, 213, 217, 221 & 222, 233, 241, 243, 251, 256, 258, 260, 262, and 264, respectively, wherein detection of the TEM protein indicates neoangiogenesis in the patient.

59. An isolated and purified nucleic acid molecule which encodes a NEM protein selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289.

60. The nucleic acid molecule of claim 59 wherein the nucleic acid molecule comprises a coding sequence as shown in SEQ ID NO: 278, 282, 284, and 288.

61. A recombinant host cell which comprises a nucleic acid according to claim 59.

62. An isolated and purified NEM protein selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, respectively.

63. An isolated molecule comprising an antibody variable region which specifically binds to a NEM protein selected from the group

consisting of: 14, 22, 23, and 33, as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289.

64. A method of inhibiting neoangiogenesis, comprising:

administering to a subject in need thereof an effective amount of a NEM protein selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, whereby neoangiogenesis is inhibited.

65. A method to identify candidate drugs for treating tumors, comprising:

contacting cells which express one or more TEM genes selected from the group consisting of: 1, 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 30, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 195, 197, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221 & 222, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 256, 258, 260, 262, 266, 268, 270, 272, and 274, respectively, with a test compound;

determining expression of said one or more TEM genes by hybridization of mRNA of said cells to a nucleic acid probe which is complementary to said mRNA; and

identifying a test compound as a candidate drug for treating tumors if it decreases expression of said one or more TEM genes.

66. The method of claim 65 wherein the cells are endothelial cells.

67. The method of claim 65 wherein the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more TEMs.

68. A method to identify candidate drugs for treating tumors, comprising:

contacting cells which express one or more TEM proteins selected from the group consisting of: 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 30, 31, 33, 35, 36, 37, 38, 39, 41,

42, 44, 45, and 46 as shown in SEQ ID NO: 198, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275, respectively, with a test compound;

determining amount of said one or more TEM proteins in said cells; and

identifying a test compound as a candidate drug for treating tumors if it decreases the amount of one or more TEM proteins in said cells.

69. The method of claim 69 wherein the cells are endothelial cells.

70. The method of claim 69 wherein the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more TEMs.

71. A method to identify candidate drugs for treating tumors, comprising:

contacting cells which express one or more TEM proteins selected from the group consisting of: 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 198, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275 respectively, with a test compound;

determining activity of said one or more TEM proteins in said cells; and

identifying a test compound as a candidate drug for treating tumors if it decreases the activity of of one more TEM proteins in said cells.

72. The method of claim 72 wherein the cells are endothelial cells.

73. The method of claim 72 wherein the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more TEMs.

74. A method to identify candidate drugs for treating patients bearing tumors, comprising:

contacting a test compound with recombinant host cells which are transfected with an expression construct which encodes one or more TEM proteins selected from the group consisting of 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 198, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275, respectively;

determining proliferation of said cells; and

identifying a test compound which inhibits proliferation of said cells as a candidate drug for treating patients bearing tumors.

75. A method to identify candidate drugs for treating tumors, comprising:

contacting cells which express one or more NEM genes selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 278, 282, 284, and 288, respectively, with a test compound;

determining expression of said one or more NEM genes by hybridization of mRNA of said cells to a nucleic acid probe which is complementary to said mRNA; and

identifying a test compound as a candidate drug for treating tumors if it increases expression of said one or more NEM genes.

76. The method of claim 76 wherein the cells are endothelial cells.

77. The method of claim 76 wherein the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more NEMs.

78. A method to identify candidate drugs for treating tumors,
comprising:

contacting cells which express one or more NEM proteins
selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ
ID NO: 279, 283, 285, 286, 287, and 289, with a test compound;

determining amount of said one or more NEM proteins in
said cells; and

identifying a test compound as a candidate drug for
treating tumors if it increases the amount of one more NEM proteins in
said cells.

79. The method of claim 79 wherein the cells are endothelial cells.

80. The method of claim 79 wherein the cells are recombinant host
cells which are transfected with an expression construct which
encodes said one or more NEMs.

81. A method to identify candidate drugs for treating tumors, comprising:

contacting cells which express one or more NEM proteins selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, with a test compound;

determining activity of said one or more NEM proteins in said cells; and

identifying a test compound as a candidate drug for treating tumors if it increases the activity of one or more NEM proteins in said cells.

82. The method of claim 81 wherein the cells are endothelial cells.

83. The method of claim 81 wherein the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more NEMs.

84. A method to identify candidate drugs for treating patients bearing tumors, comprising:

contacting a test compound with recombinant host cells which are transfected with an expression construct which encodes one or more NEM proteins selected from the group consisting of 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289;

determining proliferation of said cells; and

identifying a test compound which stimulates proliferation of said cells as a candidate drug for treating patients bearing tumors.

85. A method for identification of a ligand involved in endothelial cell regulation, comprising:

contacting a test compound with a human transmembrane TEM protein selected from the group consisting of 1, 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 196,

198, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228,
230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257,
259, 261, 263, 267, 269, 271, 273, and 275;

determining binding of a test compound to the human transmembrane protein, wherein a test compound which binds to the protein is identified as a ligand involved in endothelial cell regulation.

86. A method of inducing an immune response in a mammal,
comprising:
administering to the mammal a cell which expresses a
transmembrane protein selected from the group consisting of: TEM 1, 9,
13, 17, 19, 22, 30, and 44 as shown in SEQ ID NO: 196, 212, 220, 230,
232, 238, 250 and 271 , respectively, wherein the cell is a recombinant cell
which comprises a vector encoding said transmembrane protein, or the cell
is a fusion of a dendritic cell and a tumor endothelium cell, whereby an
immune response to the human transmembrane protein is induced in the
mammal.

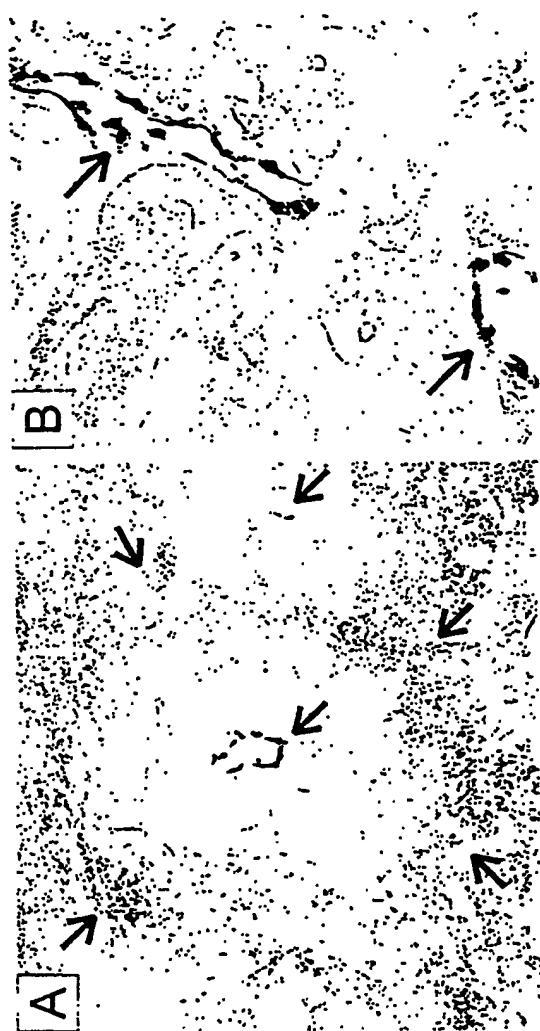


Figure 1

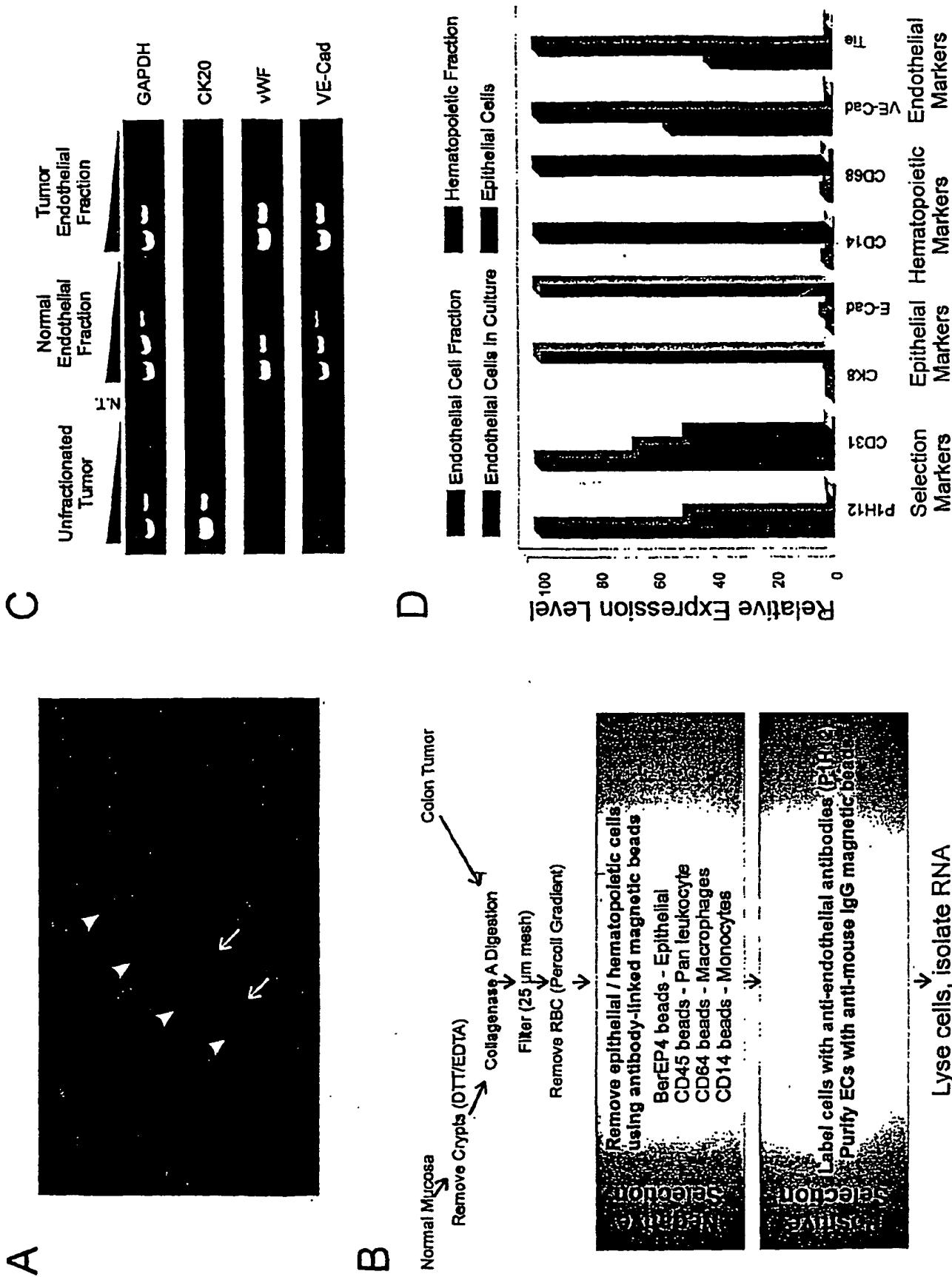


Figure 2

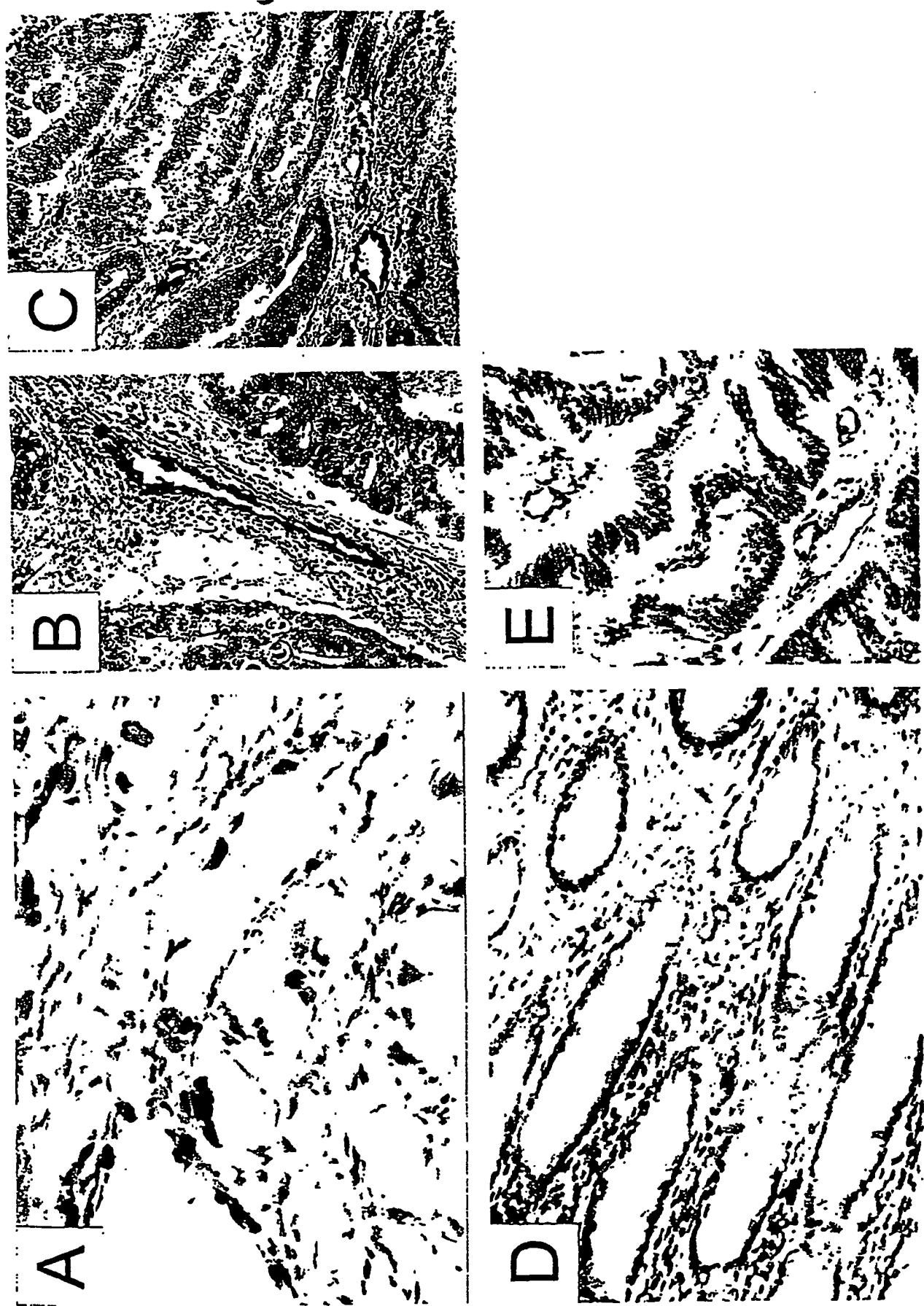


Figure 3

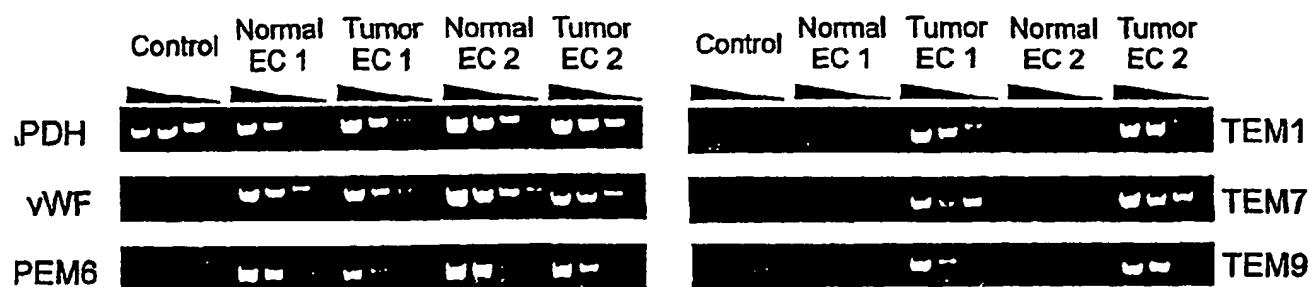
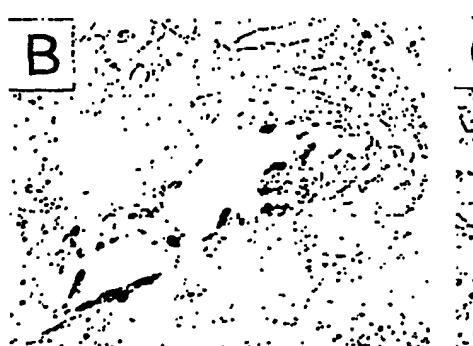
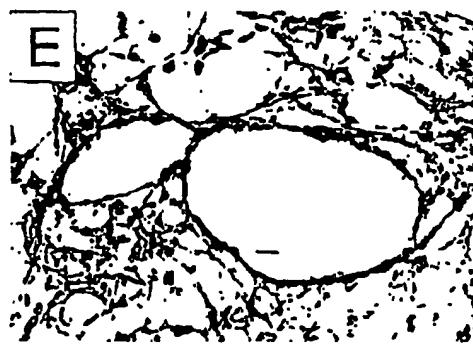
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Figure 4

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Kenneth Kinzler

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 Arg Leu Leu Trp Ile Gly Leu Gln Arg Gln Ala Arg Gln Cys Gln Leu
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 Gln Arg Pro Leu Arg Gly Phe Thr Trp Thr Thr Gly Asp Gln Asp Thr
 100 105 110
 Ala Phe Thr Asn Trp Ala Gln Pro Ala Ser Gly Gly Pro Cys Pro Ala
 115 120 125
 Gln Arg Cys Val Ala Leu Glu Ala Ser Gly Glu His Arg Trp Leu Glu
 130 135 140
 Gly Ser Cys Thr Leu Ala Val Asp Gly Tyr Leu Cys Gln Phe Gly Phe
 145 150 155 160
 Glu Gly Ala Cys Pro Ala Leu Gln Asp Glu Ala Gly Gln Ala Gly Pro
 165 170 175
 Ala Val Tyr Thr Thr Pro Phe His Leu Val Ser Thr Glu Phe Glu Trp
 180 185 190
 Leu Pro Phe Gly Ser Val Ala Ala Val Gln Cys Gln Ala Gly Arg Gly

195	200	205
Ala Ser Leu Leu Cys Val Lys Gln Pro Glu Gly Gly Val Gly Trp Ser		
210	215	220
Arg Ala Gly Pro Leu Cys Leu Gly Thr Gly Cys Ser Pro Asp Asn Gly		
225	230	235
Gly Cys Glu His Glu Cys Val Glu Val Asp Gly His Val Ser Cys		
245	250	255
Arg Cys Thr Glu Gly Phe Arg Leu Ala Ala Asp Gly Arg Ser Cys Glu		
260	265	270
Asp Pro Cys Ala Gln Ala Pro Cys Glu Gln Gln Cys Glu Pro Gly Gly		
275	280	285
Pro Gln Gly Tyr Ser Cys His Cys Arg Leu Gly Phe Arg Pro Ala Glu		
290	295	300
Asp Asp Pro His Arg Cys Val Asp Thr Asp Glu Cys Gln Ile Ala Gly		
305	310	315
Val Cys Gln Gln Met Cys Val Asn Tyr Val Gly Gly Phe Glu Cys Tyr		
325	330	335
Cys Ser Glu Gly His Glu Leu Glu Ala Asp Gly Ile Ser Cys Ser Pro		
340	345	350
Ala Gly Ala Met Gly Ala Gln Ala Ser Gln Asp Leu Gly Asp Glu Leu		
355	360	365
Leu Asp Asp Gly Glu Asp Glu Glu Asp Glu Asp Glu Ala Trp Lys Ala		
370	375	380
Phe Asn Gly Gly Trp Thr Glu Met Pro Gly Ile Leu Trp Met Glu Pro		
385	390	395
Thr Gln Pro Pro Asp Phe Ala Leu Ala Tyr Arg Pro Ser Phe Pro Glu		
405	410	415
Asp Arg Glu Pro Gln Ile Pro Tyr Pro Glu Pro Thr Trp Pro Pro Pro		
420	425	430
Leu Ser Ala Pro Arg Val Pro Tyr His Ser Ser Val Leu Ser Val Thr		
435	440	445
Arg Pro Val Val Val Ser Ala Thr His Pro Thr Leu Pro Ser Ala His		
450	455	460
Gln Pro Pro Val Ile Pro Ala Thr His Pro Ala Leu Ser Arg Asp His		
465	470	475
Gln Ile Pro Val Ile Ala Ala Asn Tyr Pro Asp Leu Pro Ser Ala Tyr		
485	490	495
Gln Pro Gly Ile Leu Ser Val Ser His Ser Ala Gln Pro Pro Ala His		
500	505	510
Gln Pro Pro Met Ile Ser Thr Lys Tyr Pro Glu Leu Phe Pro Ala His		
515	520	525
Gln Ser Pro Met Phe Pro Asp Thr Arg Val Ala Gly Thr Gln Thr Thr		
530	535	540
Thr His Leu Pro Gly Ile Pro Pro Asn His Ala Pro Leu Val Thr Thr		
545	550	555
Leu Gly Ala Gln Leu Pro Pro Gln Ala Pro Asp Ala Leu Val Leu Arg		
565	570	575
Thr Gln Ala Thr Gln Leu Pro Ile Ile Pro Thr Ala Gln Pro Ser Leu		
580	585	590
Thr Thr Thr Ser Arg Ser Pro Val Ser Pro Ala His Gln Ile Ser Val		
595	600	605
Pro Ala Ala Thr Gln Pro Ala Ala Leu Pro Thr Leu Leu Pro Ser Gln		
610	615	620
Ser Pro Thr Asn Gln Thr Ser Pro Ile Ser Pro Thr His Pro His Ser		
625	630	635
Lys Ala Pro Gln Ile Pro Arg Glu Asp Gly Pro Ser Pro Lys Leu Ala		
645	650	655
Leu Trp Leu Pro Ser Pro Ala Pro Thr Ala Ala Pro Thr Ala Leu Gly		
660	665	670
Glu Ala Gly Leu Ala Glu His Ser Gln Arg Asp Asp Arg Trp Leu Leu		
675	680	685

Val Ala Leu Leu Val Pro Thr Cys Val Phe Leu Val Val Leu Leu Ala
 690 695 700
 Leu Gly Ile Val Tyr Cys Thr Arg Cys Gly Pro His Ala Pro Asn Lys
 705 710 715 720
 Arg Ile Thr Asp Cys Tyr Arg Trp Val Ile His Ala Gly Ser Lys Ser
 725 730 735
 Pro Thr Glu Pro Met Pro Pro Arg Gly Ser Leu Thr Gly Val Gln Thr
 740 745 750
 Cys Arg Thr Ser Val
 755

<210> 178
 <211> 278
 <212> PRT
 <213> Homo sapiens

<400> 178
 Met Pro Ala Ser Leu Ala Leu Leu Gln Pro Arg Ala Met Met Lys Thr
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 20 25 30
 Arg Met Val Val Leu Gly Ala Ser Arg Val Gly Lys Ser Ser Ile Val
 35 40 45
 Ser Arg Phe Leu Asn Gly Arg Phe Glu Asp Gln Tyr Thr Pro Thr Ile
 50 55 60
 Glu Asp Phe His Arg Lys Val Tyr Asn Ile Arg Gly Asp Met Tyr Gln
 65 70 75 80
 Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala Met Arg
 85 90 95
 Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu Val Phe Ser Leu
 100 105 110
 Asp Asn Arg Glu Ser Phe Asp Glu Val Lys Arg Leu Gln Lys Gln Ile
 115 120 125
 Leu Glu Val Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Ala Ala Glu
 130 135 140
 Leu Pro Met Val Ile Cys Gly Asn Lys Asn Asp His Gly Glu Leu Cys
 145 150 155 160
 Arg Gln Val Pro Thr Thr Glu Ala Glu Leu Leu Val Ser Gly Asp Glu
 165 170 175
 Asn Cys Ala Tyr Phe Glu Val Ser Ala Lys Lys Asn Thr Asn Val Asp
 180 185 190
 Glu Met Phe Tyr Val Leu Phe Ser Met Ala Lys Leu Pro His Glu Met
 195 200 205
 Ser Pro Ala Leu His Arg Lys Ile Ser Val Gln Tyr Gly Asp Ala Phe
 210 215 220
 His Pro Arg Pro Phe Cys Met Arg Arg Val Lys Glu Met Asp Ala Tyr
 225 230 235 240
 Gly Met Val Ser Pro Phe Ala Arg Arg Pro Ser Val Asn Ser Asp Leu
 245 250 255
 Lys Tyr Ile Lys Ala Lys Val Leu Arg Glu Gly Gln Ala Arg Glu Arg
 260 265 270
 Asp Lys Cys Thr Ile Gln
 275

<210> 179
 <211> 1002
 <212> PRT
 <213> Homo sapiens

<400> 179
 Met Arg Gly Glu Leu Trp Leu Leu Val Leu Val Leu Arg Glu Ala Ala

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Ser Gly Trp Ala Ala Lys Gly	Thr Val Arg Gly Trp	Asn Arg Arg Ala	
35	40	45	
Arg Glu Ser Pro Gly His Val	Ser Glu Pro Asp Arg	Thr Gln Leu Ser	
50	55	60	
Gln Asp Leu Gly Gly	Thr Leu Ala Met Asp Thr	Leu Pro Asp Asn	
65	70	75	80
Arg Thr Arg Val Val Glu Asp Asn His	Ser Tyr Tyr Val	Ser Arg Leu	
85	90	95	
Tyr Gly Pro Ser Glu Pro His	Ser Arg Glu Leu Trp Val	Asp Val Ala	
100	105	110	
Glu Ala Asn Arg Ser Gln Val	Lys Ile His Thr Ile	Leu Ser Asn Thr	
115	120	125	
His Arg Gln Ala Ser Arg Val	Val Leu Ser Phe Asp	Phe Pro Phe Tyr	
130	135	140	
Gly His Pro Leu Arg Gln	Ile Thr Ile Ala Thr	Gly Phe Ile Phe	
145	150	155	160
Met Gly Asp Val Ile His Arg Met	Leu Thr Ala Thr	Gln Tyr Val Ala	
165	170	175	
Pro Leu Met Ala Asn Phe Asn	Pro Gly Tyr Ser Asp Asn	Ser Thr Val	
180	185	190	
Val Tyr Phe Asp Asn Gly	Thr Val Phe Val Val	Gln Trp Asp His Val	
195	200	205	
Tyr Leu Gln Gly Trp Glu Asp	Lys Gly Ser Phe Thr	Phe Gln Ala Ala	
210	215	220	
Leu His His Asp Gly Arg Ile Val	Phe Ala Tyr Lys Glu Ile Pro	Met	
225	230	235	240
Ser Val Pro Glu Ile Ser Ser	Ser Gln His Pro Val	Lys Thr Gly Leu	
245	250	255	
Ser Asp Ala Phe Met Ile Leu Asn	Pro Ser Pro Asp Val	Pro Glu Ser	
260	265	270	
Arg Arg Arg Ser Ile Phe Glu	Tyr His Arg Ile Glu	Leu Asp Pro Ser	
275	280	285	
Lys Val Thr Ser Met Ser Ala	Val Glu Phe Thr Pro	Leu Pro Thr Cys	
290	295	300	
Leu Gln His Arg Ser Cys Asp	Ala Cys Met Ser Ser	Asp Leu Thr Phe	
305	310	315	320
Asn Cys Ser Trp Cys His Val	Leu Gln Arg Cys Ser Ser	Gly Phe Asp	
325	330	335	
Arg Tyr Arg Gln Glu Trp Asp	Gly Thr Met Gly Cys Ala	Gln Glu Ala	
340	345	350	
Glu Gly Gln Asp Val Arg Gly	Leu Pro Gly Met Arg	Thr Thr Ser	
355	360	365	
Ala Ser Pro Asp Thr Ser Phe	Ser Pro Tyr Asp Gly	Asp Leu Thr Thr	
370	375	380	
Thr Ser Ser Ser Leu Phe	Ile Asp Ser Leu Thr	Glu Asp Asp Thr	
385	390	395	400
Lys Leu Asn Pro Tyr Ala Gly	Gly Asp Gly Leu Gln Asn Asn	Leu Ser	
405	410	415	
Pro Lys Thr Lys Gly Thr Pro	Val His Leu Gly Thr Ile	Val Gly Ile	
420	425	430	
Val Leu Ala Val Leu Leu Val	Ala Ile Ile Leu Ala	Gly Ile Tyr	
435	440	445	
Ile Asn Gly His Pro Thr Ser	Asn Ala Ala Leu Phe	Phe Ile Glu Arg	
450	455	460	
Arg Pro His His Trp Pro Ala	Met Lys Phe Arg Ser	His Pro Asp His	
465	470	475	480
Ser Thr Tyr Ala Glu Val Glu	Pro Ser Gly His Glu	Lys Glu Gly Phe	
485	490	495	

Met Glu Ala Glu Gln Cys Met Arg Gly Glu Leu Trp Leu Leu Val Leu
 500 505 510
 Val Leu Arg Glu Ala Ala Arg Ala Leu Ser Pro Gln Pro Gly Ala Gly
 515 520 525
 His Asp Glu Gly Pro Gly Ser Gly Trp Ala Ala Lys Gly Thr Val Arg
 530 535 540
 Gly Trp Asn Arg Arg Ala Arg Glu Ser Pro Gly His Val Ser Glu Pro
 545 550 555 560
 Asp Arg Thr Gln Leu Ser Gln Asp Leu Gly Gly Thr Leu Ala Met
 565 570 575
 Asp Thr Leu Pro Asp Asn Arg Thr Arg Val Val Glu Asp Asn His Ser
 580 585 590
 Tyr Tyr Val Ser Arg Leu Tyr Gly Pro Ser Glu Pro His Ser Arg Glu
 595 600 605
 Leu Trp Val Asp Val Ala Glu Ala Asn Arg Ser Gln Val Lys Ile His
 610 615 620
 Thr Ile Leu Ser Asn Thr His Arg Gln Ala Ser Arg Val Val Leu Ser
 625 630 635 640
 Phe Asp Phe Pro Phe Tyr Gly His Pro Leu Arg Gln Ile Thr Ile Ala
 645 650 655
 Thr Gly Gly Phe Ile Phe Met Gly Asp Val Ile His Arg Met Leu Thr
 660 665 670
 Ala Thr Gln Tyr Val Ala Pro Leu Met Ala Asn Phe Asn Pro Gly Tyr
 675 680 685
 Ser Asp Asn Ser Thr Val Val Tyr Phe Asp Asn Gly Thr Val Phe Val
 690 695 700
 Val Gln Trp Asp His Val Tyr Leu Gln Gly Trp Glu Asp Lys Gly Ser
 705 710 715 720
 Phe Thr Phe Gln Ala Ala Leu His His Asp Gly Arg Ile Val Phe Ala
 725 730 735
 Tyr Lys Glu Ile Pro Met Ser Val Pro Glu Ile Ser Ser Ser Gln His
 740 745 750
 Pro Val Lys Thr Gly Leu Ser Asp Ala Phe Met Ile Leu Asn Pro Ser
 755 760 765
 Pro Asp Val Pro Glu Ser Arg Arg Arg Ser Ile Phe Glu Tyr His Arg
 770 775 780
 Ile Glu Leu Asp Pro Ser Lys Val Thr Ser Met Ser Ala Val Glu Phe
 785 790 795 800
 Thr Pro Leu Pro Thr Cys Leu Gln His Arg Ser Cys Asp Ala Cys Met
 805 810 815
 Ser Ser Asp Leu Thr Phe Asn Cys Ser Trp Cys His Val Leu Gln Arg
 820 825 830
 Cys Ser Ser Gly Phe Asp Arg Tyr Arg Gln Glu Trp Met Asp Tyr Gly
 835 840 845
 Cys Ala Gln Glu Ala Glu Gly Arg Met Cys Glu Asp Phe Gln Asp Glu
 850 855 860
 Asp His Asp Ser Ala Ser Pro Asp Thr Ser Phe Ser Pro Tyr Asp Gly
 865 870 875 880
 Asp Leu Thr Thr Ser Ser Leu Phe Ile Asp Ser Leu Thr Thr
 885 890 895
 Glu Asp Asp Thr Lys Leu Asn Pro Tyr Ala Gly Gly Asp Gly Leu Gln
 900 905 910
 Asn Asn Leu Ser Pro Lys Thr Lys Gly Thr Pro Val His Leu Gly Thr
 915 920 925
 Ile Val Gly Ile Val Leu Ala Val Leu Leu Val Ala Ala Ile Ile Leu
 930 935 940
 Ala Gly Ile Tyr Ile Asn Gly His Pro Thr Ser Asn Ala Ala Leu Phe
 945 950 955 960
 Phe Ile Glu Arg Arg Pro His His Trp Pro Ala Met Lys Phe Arg Ser
 965 970 975
 His Pro Asp His Ser Thr Tyr Ala Glu Val Glu Pro Ser Gly His Glu

980	985	990
Lys Glu Gly Phe Met Glu Ala Glu Gln Cys		
995	1000	

<210> 180
<211> 5680
<212> DNA
<213> Homo sapiens

<400> 180

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ctgccccta tccatccgca gctcaagtg ctggggggag cggcccaagg ggctgagcgg	180
cggcgccct ggcccggtc ggccgggggt ggtgtcagc ggccgggacc tcccgagcc	240
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cgccagcaag aagggtggaga tcgtggctg ggagacctt gcctccact gccccggccga	1080
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<210> 181
<211> 2157
<212> DNA
<213> Homo sapiens

<400> 181

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gatggcagt	atggaggttac	tcagggcttc	cctcacacag	aggaggaggt	ggaagttgat	180
tcacacgcgt	acagccacag	gtggaaaaga	aacttggact	ttctcaaggc	ggtagacacg	240
aaccgagcaa	gcgtcgccca	agactctct	gagcccaaga	gcttcacaga	cctgtgtctg	300
gatgatgggc	aggacaataa	cactcagatc	gaggaggata	cagaccacaa	ttactatata	360
tctcgaatat	atggtccatc	tgattctgcc	agccgggatt	tatgggtgaa	catagaccaa	420
atggaaaaaa	ataaaagtgaa	gattcatgga	atattgtcca	atactcatcg	gcaagctgca	480

agagtgaatc	tgtccttcga	ttttccattt	tatggccact	tcctacgtga	aatcaactgtg	540
gcaaccgggg	gtttcatata	cactggagaa	gtcgtaatc	gaatgctaac	agccacacag	600
tacatagcac	ctttaatgc	aaatttcgtat	cccagtgtat	ccagaaattc	aactgtcaga	660
tatTTGATA	atggcacagc	acttgtggc	cagtggacc	atgtacatct	ccaggataat	720
tataacctgg	gaagcttcac	attccaggca	accctgccta	tggatggacg	aatcatctt	780
ggatACAAG	aaattcctgt	cttggtcaca	cagataagtt	caaccaatca	tccagtgaaa	840
gtcggactgt	ccgatgcatt	tgtcgttgc	cacaggatcc	aacaaattcc	caatgttcga	900
agaagaacaa	tttatgaata	ccaccgagta	gagctacaaa	tgtaaaaaat	taccaacatt	960
tcggctgtgg	agatgacccc	attacccaca	tgccctcagt	ttaacagatg	tggccctgt	1020
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<212> DNA

<213> Mus musculus

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<210> 186

<211> 5220

<212> DNA

<213> Mus musculus

<400> 186

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ctgctgc当地	ccctggcgt	gctctgggg	ttctggcccc	tctgc当地	agtgc当地	1320

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acggagg	ttt	ttt	ttt	ttt	ttt	4200
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agtgtt	ttt	ttt	ttt	ttt	ttt	4320
gcttt	ttt	ttt	ttt	ttt	ttt	4380
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cctgg	ttt	ttt	ttt	ttt	ttt	4500
caaag	ttt	ttt	ttt	ttt	ttt	4560
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<210> 187
<211> 564
<212> PRT
<213> Homo sapiens

<400> 187
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35 40 45
Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
50 55 60
Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
65 70 75 80
Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
85 90 95
Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
100 105 110
Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
115 120 125
Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
130 135 140
Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
145 150 155 160
Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
165 170 175
Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
180 185 190
Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
195 200 205
Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
210 215 220
Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
225 230 235 240
Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
245 250 255
Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
260 265 270
Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
275 280 285
Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
290 295 300
Phe Ile Ser Ser Ser Val Ile Ile Thr Thr His Cys Ser Asp Gly
305 310 315 320
Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
325 330 335
Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys
340 345 350
Glu Val Pro Pro Pro Ala Glu Glu Ser Glu Glu Asp Asp Asp
355 360 365
Gly Leu Pro Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly

370	375	380
Gly Arg Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu		
385	390	395
Lys Gly Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala		400
405	410	415
Arg Val Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn		
420	425	430
Leu Asn Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser		
435	440	445
Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly		
450	455	460
Tyr Asp Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg		
465	470	475
Cys Ile Asn Phe Thr Arg Val Lys Asn Asn Gln Pro Ala Lys Tyr Pro		480
485	490	495
Leu Asn Asn Ala Tyr His Thr Ser Ser Pro Pro Pro Ala Pro Ile Tyr		
500	505	510
Thr Pro Pro Pro Ala Pro His Cys Pro Pro Pro Pro Pro Ser Ala		
515	520	525
Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro		
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Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro		
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Arg Pro Ser Val		560

<210> 188
<211> 1331
<212> PRT
<213> Homo sapiens

<400> 188		
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20	25	30
Ser Ile Arg Ser Cys Lys Cys Ser Gly Glu Arg Pro Lys Gly Leu Ser		
35	40	45
Gly Gly Val Pro Gly Pro Ala Arg Arg Val Val Cys Ser Gly Gly		
50	55	60
Asp Leu Pro Glu Pro Pro Glu Pro Gly Leu Leu Pro Asn Gly Thr Val		
65	70	75
80		
Thr Leu Leu Leu Ser Asn Asn Lys Ile Thr Gly Leu Arg Asn Gly Ser		
85	90	95
Phe Leu Gly Leu Ser Leu Leu Glu Lys Leu Asp Leu Arg Asn Asn Ile		
100	105	110
Ile Ser Thr Val Gln Pro Gly Ala Phe Leu Gly Leu Glu Leu Lys		
115	120	125
Arg Leu Asp Leu Ser Asn Asn Arg Ile Gly Cys Leu Thr Ser Glu Thr		
130	135	140
Phe Gln Gly Leu Pro Arg Leu Leu Arg Leu Asn Ile Ser Gly Asn Ile		
145	150	155
160		
Phe Ser Ser Leu Gln Pro Gly Val Phe Asp Glu Leu Pro Ala Leu Lys		
165	170	175
Val Val Asp Leu Gly Thr Glu Phe Leu Thr Cys Asp Cys His Leu Arg		
180	185	190
Trp Leu Leu Pro Trp Ala Gln Asn Arg Ser Leu Gln Leu Ser Glu His		
195	200	205
Thr Leu Cys Ala Tyr Pro Ser Ala Leu His Ala Gln Ala Leu Gly Ser		
210	215	220
Leu Gln Glu Ala Gln Leu Cys Cys Glu Gly Ala Leu Glu Leu His Thr		

225	230	235	240
His His Leu Ile Pro Ser Leu Arg Gln Val Val Phe Gln Gly Asp Arg			
245	250	255	
Leu Pro Phe Gln Cys Ser Ala Ser Tyr Leu Gly Asn Asp Thr Arg Ile			
260	265	270	
Arg Trp Tyr His Asn Arg Ala Pro Val Glu Gly Asp Glu Gln Ala Gly			
275	280	285	
Ile Leu Leu Ala Glu Ser Leu Ile His Asp Cys Thr Phe Ile Thr Ser			
290	295	300	
Glu Leu Thr Leu Ser His Ile Gly Val Trp Ala Ser Gly Glu Trp Glu			
305	310	315	320
Cys Thr Val Ser Met Ala Gln Gly Asn Ala Ser Lys Lys Val Glu Ile			
325	330	335	
Val Val Leu Glu Thr Ser Ala Ser Tyr Cys Pro Ala Glu Arg Val Ala			
340	345	350	
Asn Asn Arg Gly Asp Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr			
355	360	365	
Ala Tyr Gln Ser Cys Leu Gln Tyr Pro Phe Thr Ser Val Pro Leu Gly			
370	375	380	
Gly Gly Ala Pro Gly Thr Arg Ala Ser Arg Arg Cys Asp Arg Ala Gly			
385	390	395	400
Arg Trp Glu Pro Gly Asp Tyr Ser His Cys Leu Tyr Thr Asn Asp Ile			
405	410	415	
Thr Arg Val Leu Tyr Thr Phe Val Leu Met Pro Ile Asn Ala Ser Asn			
420	425	430	
Ala Leu Thr Leu Ala His Gln Leu Arg Val Tyr Thr Ala Glu Ala Ala			
435	440	445	
Ser Phe Ser Asp Met Met Asp Val Val Tyr Val Ala Gln Met Ile Gln			
450	455	460	
Lys Phe Leu Gly Tyr Val Asp Gln Ile Lys Glu Leu Val Glu Val Met			
465	470	475	480
Val Asp Met Ala Ser Asn Leu Met Leu Val Asp Glu His Leu Leu Trp			
485	490	495	
Leu Ala Gln Arg Glu Asp Lys Ala Cys Ser Arg Ile Val Gly Ala Leu			
500	505	510	
Glu Arg Ile Gly Gly Ala Ala Leu Ser Pro His Ala Gln His Ile Ser			
515	520	525	
Val Asn Ala Arg Asn Val Ala Leu Glu Ala Tyr Leu Ile Lys Pro His			
530	535	540	
Ser Tyr Val Gly Leu Thr Cys Thr Ala Phe Gln Arg Arg Glu Gly Gly			
545	550	555	560
Val Pro Gly Thr Arg Pro Gly Ser Pro Gly Gln Asn Pro Pro Pro Glu			
565	570	575	
Pro Glu Pro Pro Ala Asp Gln Gln Leu Arg Phe Arg Cys Thr Thr Gly			
580	585	590	
Arg Pro Asn Val Ser Leu Ser Ser Phe His Ile Lys Asn Ser Val Ala			
595	600	605	
Leu Ala Ser Ile Gln Leu Pro Pro Ser Leu Phe Ser Ser Leu Pro Ala			
610	615	620	
Ala Leu Ala Pro Pro Val Pro Pro Asp Cys Thr Leu Gln Leu Leu Val			
625	630	635	640
Phe Arg Asn Gly Arg Leu Phe His Ser His Ser Asn Thr Ser Arg Pro			
645	650	655	
Gly Ala Ala Gly Pro Gly Lys Arg Arg Gly Val Ala Thr Pro Val Ile			
660	665	670	
Phe Ala Gly Thr Ser Gly Cys Gly Val Gly Asn Leu Thr Glu Pro Val			
675	680	685	
Ala Val Ser Leu Arg His Trp Ala Glu Gly Ala Glu Pro Val Ala Ala			
690	695	700	
Trp Trp Ser Gln Glu Gly Pro Gly Glu Ala Gly Gly Trp Thr Ser Glu			
705	710	715	720

Gly Cys Gin Leu Arg Ser Ser Gln Pro Asn Val Ser Ala Leu His Cys
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 Gln His Leu Gly Asn Val Ala Val Leu Met Glu Leu Ser Ala Phe Pro
 740 745 750
 Arg Glu Val Gly Gly Ala Gly Leu His Pro Val Val Tyr Pro
 755 760 765
 Cys Thr Ala Leu Leu Leu Cys Leu Phe Ala Thr Ile Ile Thr Tyr
 770 775 780
 Ile Leu Asn His Ser Ser Ile Arg Val Ser Arg Lys Gly Trp His Met
 785 790 795 800
 Leu Leu Asn Leu Cys Phe His Ile Ala Met Thr Ser Ala Val Phe Ala
 805 810 815
 Gly Gly Ile Thr Leu Thr Asn Tyr Gln Met Val Cys Gln Ala Val Gly
 820 825 830
 Ile Thr Leu His Tyr Ser Ser Leu Ser Thr Leu Leu Trp Met Gly Val
 835 840 845
 Lys Ala Arg Val Leu His Lys Glu Leu Thr Trp Arg Ala Pro Pro Pro
 850 855 860
 Gln Glu Gly Asp Pro Ala Leu Pro Thr Pro Ser Pro Met Leu Arg Phe
 865 870 875 880
 Tyr Leu Ile Ala Gly Gly Ile Pro Leu Ile Ile Cys Gly Ile Thr Ala
 885 890 895
 Ala Val Asn Ile His Asn Tyr Arg Asp His Ser Pro Tyr Cys Trp Leu
 900 905 910
 Val Trp Arg Pro Ser Leu Gly Ala Phe Tyr Ile Pro Val Ala Leu Ile
 915 920 925
 Leu Leu Ile Thr Trp Ile Tyr Phe Leu Cys Ala Gly Leu Arg Leu Arg
 930 935 940
 Gly Pro Leu Ala Gln Asn Pro Lys Ala Gly Asn Ser Arg Ala Ser Leu
 945 950 955 960
 Glu Ala Gly Glu Glu Leu Arg Gly Ser Thr Arg Leu Arg Gly Ser Gly
 965 970 975
 Pro Leu Leu Ser Asp Ser Gly Ser Leu Leu Ala Thr Gly Ser Ala Arg
 980 985 990
 Val Gly Thr Pro Gly Pro Pro Glu Asp Gly Asp Ser Leu Tyr Ser Pro
 995 1000 1005
 Gly Val Gln Leu Gly Ala Leu Val Thr Thr His Phe Leu Tyr Leu Ala
 1010 1015 1020
 Met Trp Ala Cys Gly Ala Leu Ala Val Ser Gln Arg Trp Leu Pro Arg
 1025 1030 1035 1040
 Val Val Cys Ser Cys Leu Tyr Gly Val Ala Ala Ser Ala Leu Gly Leu
 1045 1050 1055
 Phe Val Phe Thr His His Cys Ala Arg Arg Arg Asp Val Arg Ala Ser
 1060 1065 1070
 Trp Arg Ala Cys Cys Pro Pro Ala Ser Pro Ala Ala Pro His Ala Pro
 1075 1080 1085
 Pro Arg Ala Leu Pro Ala Ala Ala Glu Asp Gly Ser Pro Val Phe Gly
 1090 1095 1100
 Glu Gly Pro Pro Ser Leu Lys Ser Ser Pro Ser Gly Ser Ser Gly His
 1105 1110 1115 1120
 Pro Leu Ala Leu Gly Pro Cys Lys Leu Thr Asn Leu Gln Leu Ala Gln
 1125 1130 1135
 Ser Gln Val Cys Glu Ala Gly Ala Ala Ala Gly Gly Glu Gly Glu Pro
 1140 1145 1150
 Glu Pro Ala Gly Thr Arg Gly Asn Leu Ala His Arg His Pro Asn Asn
 1155 1160 1165
 Val His His Gly Arg Arg Ala His Lys Ser Arg Ala Lys Gly His Arg
 1170 1175 1180
 Ala Gly Glu Ala Cys Gly Lys Asn Arg Leu Lys Ala Leu Arg Gly Gly
 1185 1190 1195 1200
 Ala Ala Gly Ala Leu Glu Leu Leu Ser Ser Glu Ser Gly Ser Leu His

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Asn Ser Pro Thr Asp Ser Tyr Leu Gly Ser Ser Arg Asn Ser Pro Gly			
1220	1225	1230	
Ala Gly Leu Gln Leu Glu Gly Glu Pro Met Leu Thr Pro Ser Glu Gly			
1235	1240	1245	
Ser Asp Thr Ser Ala Ala Pro Leu Ser Glu Ala Gly Arg Ala Gly Gln			
1250	1255	1260	
Arg Arg Ser Ala Ser Arg Asp Ser Leu Lys Gly Gly Gly Ala Leu Glu			
1265	1270	1275	1280
Lys Glu Ser His Arg Arg Ser Tyr Pro Leu Asn Ala Ala Ser Leu Asn			
1285	1290	1295	
Gly Ala Pro Lys Gly Lys Tyr Asp Asp Val Thr Leu Met Gly Ala			
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Glu Val Ala Ser Gly Gly Cys Met Lys Thr Gly Leu Trp Lys Ser Glu			
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Thr Thr Val			
1330			

<210> 189

<211> 529

<212> PRT

<213> Homo sapiens

<400> 189

Met Ala Arg Phe Pro Lys Ala Asp Leu Ala Ala Gly Val Met Leu			
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20	25	30	
Gly Asp Gln Ile Leu Asp Trp Gln Tyr Gly Val Thr Gln Ala Phe Pro			
35	40	45	
His Thr Glu Glu Val Glu Val Asp Ser His Ala Tyr Ser His Arg			
50	55	60	
Trp Lys Arg Asn Leu Asp Phe Leu Lys Ala Val Asp Thr Asn Arg Ala			
65	70	75	80
Ser Val Gly Gln Asp Ser Pro Glu Pro Arg Ser Phe Thr Asp Leu Leu			
85	90	95	
Leu Asp Asp Gly Gln Asp Asn Asn Thr Gln Ile Glu Glu Asp Thr Asp			
100	105	110	
His Asn Tyr Tyr Ile Ser Arg Ile Tyr Gly Pro Ser Asp Ser Ala Ser			
115	120	125	
Arg Asp Leu Trp Val Asn Ile Asp Gln Met Glu Lys Asp Lys Val Lys			
130	135	140	
Ile His Gly Ile Leu Ser Asn Thr His Arg Gln Ala Ala Arg Val Asn			
145	150	155	160
Leu Ser Phe Asp Phe Pro Phe Tyr Gly His Phe Leu Arg Glu Ile Thr			
165	170	175	
Val Ala Thr Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met			
180	185	190	
Leu Thr Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro			
195	200	205	
Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala			
210	215	220	
Leu Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu			
225	230	235	240
Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile			
245	250	255	
Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr			
260	265	270	
Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His			
275	280	285	
Arg Ile Gln Gln Ile Pro Asn Val Arg Arg Thr Ile Tyr Glu Tyr			

290	295	300
His Arg Val Glu Leu Gln Met Ser Lys Ile Thr Asn Ile Ser Ala Val		
305	310	315 320
Glu Met Thr Pro Leu Pro Thr Cys Leu Gln Phe Asn Arg Cys Gly Pro		
	325	330 335
Cys Val Ser Ser Gln Ile Gly Phe Asn Cys Ser Trp Cys Ser Lys Leu		
	340	345 350
Gln Arg Cys Ser Ser Gly Phe Asp Arg His Arg Gln Asp Trp Val Asp		
	355	360 365
Ser Gly Cys Pro Glu Glu Ser Lys Glu Lys Met Cys Glu Asn Thr Glu		
	370	375 380
Pro Val Glu Thr Ser Ser Arg Thr Thr Thr Ile Gly Ala Thr Thr		
	385	390 395 400
Thr Gln Phe Arg Val Leu Thr Thr Arg Arg Ala Val Thr Ser Gln		
	405	410 415
Phe Pro Thr Ser Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu His		
	420	425 430
Leu Lys Asp Asn Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys Lys		
	435	440 445
Gly Gly Thr Leu His Ala Gly Leu Ile Val Gly Ile Leu Ile Leu Val		
	450	455 460
Leu Ile Val Ala Thr Ala Ile Leu Val Thr Val Tyr Met Tyr His His		
	465	470 475 480
Pro Thr Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser Arg		
	485	490 495
Trp Pro Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala Tyr Ala		
	500	505 510
Glu Val Glu Pro Val Gly Glu Lys Glu Gly Phe Ile Val Ser Glu Gln		
	515	520 525
Cys		

<210> 190
 <211> 765
 <212> PRT
 <213> Mus musculus

<400> 190	
Met Leu Leu Arg Leu Leu Leu Ala Trp Val Ala Ala Val Pro Ala Leu	
1 5 10 15	
Gly Gln Val Pro Trp Thr Pro Glu Pro Arg Ala Ala Cys Gly Pro Ser	
	20 25 30
Ser Cys Tyr Ala Leu Phe Pro Arg Arg Arg Thr Phe Leu Glu Ala Trp	
	35 40 45
Arg Ala Cys Arg Glu Leu Gly Gly Asn Leu Ala Thr Pro Arg Thr Pro	
	50 55 60
Glu Glu Ala Gln Arg Val Asp Ser Leu Val Gly Val Gly Pro Ala Asn	
	65 70 75 80
Gly Leu Leu Trp Ile Gly Leu Gln Arg Gln Ala Arg Gln Cys Gln Pro	
	85 90 95
Gln Arg Pro Leu Arg Gly Phe Ile Trp Thr Gly Asp Gln Asp Thr	
	100 105 110
Ala Phe Thr Asn Trp Ala Gln Pro Ala Thr Glu Gly Pro Cys Pro Ala	
	115 120 125
Gln Arg Cys Ala Ala Leu Glu Ala Ser Gly Glu His Arg Trp Leu Glu	
	130 135 140
Gly Ser Cys Thr Leu Ala Val Asp Gly Tyr Leu Cys Gln Phe Gly Phe	
	145 150 155 160
Glu Gly Ala Cys Pro Ala Leu Pro Leu Glu Val Gly Gln Ala Gly Pro	
	165 170 175
Ala Val Tyr Thr Pro Phe Asn Leu Val Ser Ser Glu Phe Glu Trp	

	180	185	190
Leu Pro Phe Gly Ser Val Ala Ala Val Gln Cys Gln Ala		Gly Arg Gly	
195	200	205	
Ala Ser Leu Leu Cys Val Lys Gln Pro Ser Gly Gly Val		Gly Trp Ser	
210	215	220	
Gln Thr Gly Pro Leu Cys Pro Gly Thr Gly Cys Gly Pro Asp Asn Gly			
225	230	235	240
Gly Cys Glu His Glu Cys Val Glu Glu Val Asp Gly Ala Val Ser Cys			
245	250	255	
Arg Cys Ser Glu Gly Phe Arg Leu Ala Ala Asp Gly His Ser Cys Glu			
260	265	270	
Asp Pro Cys Ala Gln Ala Pro Cys Glu Gln Gln Cys Glu Pro Gly Gly			
275	280	285	
Pro Gln Gly Tyr Ser Cys His Cys Arg Leu Gly Phe Arg Pro Ala Glu			
290	295	300	
Asp Asp Pro His Arg Cys Val Asp Thr Asp Glu Cys Gln Ile Ala Gly			
305	310	315	320
Val Cys Gln Gln Met Cys Val Asn Tyr Val Gly Gly Phe Glu Cys Tyr			
325	330	335	
Cys Ser Glu Gly His Glu Leu Glu Ala Asp Gly Ile Ser Cys Ser Pro			
340	345	350	
Ala Gly Ala Met Gly Ala Gln Ala Ser Gln Asp Leu Arg Asp Glu Leu			
355	360	365	
Leu Asp Asp Gly Glu Glu Gly Glu Asp Glu Glu Glu Pro Trp Glu Asp			
370	375	380	
Phe Asp Gly Thr Trp Thr Glu Glu Gln Gly Ile Leu Trp Leu Ala Pro			
385	390	395	400
Thr His Pro Pro Asp Phe Gly Leu Pro Tyr Arg Pro Asn Phe Pro Gln			
405	410	415	
Asp Gly Glu Pro Gln Arg Leu His Leu Glu Pro Thr Trp Pro Pro Pro			
420	425	430	
Leu Ser Ala Pro Arg Gly Pro Tyr His Ser Ser Val Val Ser Ala Thr			
435	440	445	
Arg Pro Met Val Ile Ser Ala Thr Arg Pro Thr Leu Pro Ser Ala His			
450	455	460	
Lys Thr Ser Val Ile Ser Ala Thr Arg Pro Pro Leu Ser Pro Val His			
465	470	475	480
Pro Pro Ala Met Ala Pro Ala Thr Pro Pro Ala Val Phe Ser Glu His			
485	490	495	
Gln Ile Pro Lys Ile Lys Ala Asn Tyr Pro Asp Leu Pro Phe Gly His			
500	505	510	
Lys Pro Gly Ile Thr Ser Ala Thr His Pro Ala Arg Ser Pro Pro Tyr			
515	520	525	
Gln Pro Pro Ile Ile Ser Thr Asn Tyr Pro Gln Val Phe Pro Pro His			
530	535	540	
Gln Ala Pro Met Ser Pro Asp Thr His Thr Ile Thr Tyr Leu Pro Pro			
545	550	555	560
Val Pro Pro His Leu Asp Pro Gly Asp Thr Thr Ser Lys Ala His Gln			
565	570	575	
His Pro Leu Leu Pro Asp Ala Pro Gly Ile Arg Thr Gln Ala Pro Gln			
580	585	590	
Leu Ser Val Ser Ala Leu Gln Pro Pro Leu Pro Thr Asn Ser Arg Ser			
595	600	605	
Ser Val His Glu Thr Pro Val Pro Ala Ala Asn Gln Pro Pro Ala Phe			
610	615	620	
Pro Ser Ser Pro Leu Pro Pro Gln Arg Pro Thr Asn Gln Thr Ser Ser			
625	630	635	640
Ile Ser Pro Thr His Ser Tyr Ser Arg Ala Pro Leu Val Pro Arg Glu			
645	650	655	
Gly Val Pro Ser Pro Lys Ser Val Pro Gln Leu Pro Ser Val Pro Ser			
660	665	670	

Thr Ala Ala Pro Thr Ala Leu Ala Glu Ser Gly Leu Ala Gly Gln Ser
 675 680 685
 Gln Arg Asp Asp Arg Trp Leu Leu Val Ala Leu Leu Val Pro Thr Cys
 690 695 700
 Val Phe Leu Val Val Leu Leu Ala Leu Gly Ile Val Tyr Cys Thr Arg
 705 710 715 720
 Cys Gly Ser His Ala Pro Asn Lys Arg Ile Thr Asp Cys Tyr Arg Trp
 725 730 735
 Val Thr His Ala Gly Asn Lys Ser Ser Thr Glu Pro Met Pro Pro Arg
 740 745 750
 Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr Ser Val
 755 760 765

<210> 191
 <211> 1329
 <212> PRT
 <213> Mus musculus

<400> 191
 Met Pro Val Pro Pro Ala Arg Leu Leu Leu Pro Leu Leu Pro Cys
 1 5 10 15
 Leu Leu Leu Ala Pro Gly Thr Arg Gly Ala Pro Gly Cys Pro Val
 20 25 30
 Pro Ile Arg Gly Cys Lys Cys Ser Gly Glu Arg Pro Lys Gly Leu Ser
 35 40 45
 Gly Gly Ala His Asn Pro Ala Arg Arg Arg Val Val Cys Gly Gly
 50 55 60
 Asp Leu Pro Glu Pro Pro Asp Pro Gly Leu Leu Pro Asn Gly Thr Ile
 65 70 75 80
 Thr Leu Leu Leu Ser Asn Asn Lys Ile Thr Gly Leu Arg Asn Gly Ser
 85 90 95
 Phe Leu Gly Leu Ser Leu Leu Glu Lys Leu Asp Leu Arg Ser Asn Val
 100 105 110
 Ile Ser Thr Val Gln Pro Gly Ala Phe Leu Gly Leu Gly Glu Leu Lys
 115 120 125
 Arg Leu Asp Leu Ser Asn Asn Arg Ile Gly Cys Leu Thr Ser Glu Thr
 130 135 140
 Phe Gln Gly Leu Pro Arg Leu Leu Arg Leu Asn Ile Ser Gly Asn Ile
 145 150 155 160
 Tyr Ser Ser Leu Gln Pro Gly Val Phe Asp Glu Leu Pro Ala Leu Lys
 165 170 175
 Ile Val Asp Phe Gly Thr Glu Phe Leu Thr Cys Asp Cys Arg Leu Arg
 180 185 190
 Trp Leu Leu Pro Trp Ala Arg Asn His Ser Leu Gln Leu Ser Glu Arg
 195 200 205
 Thr Leu Cys Ala Tyr Pro Ser Ala Leu His Ala His Ala Leu Ser Ser
 210 215 220
 Leu Gln Glu Ser Gln Leu Arg Cys Glu Gly Ala Leu Glu Leu His Thr
 225 230 235 240
 His Tyr Leu Ile Pro Ser Leu Arg Gln Val Val Phe Gln Gly Asp Arg
 245 250 255
 Leu Pro Phe Gln Cys Ser Ala Ser Tyr Leu Gly Asn Asp Thr Arg Ile
 260 265 270
 His Trp Tyr His Asn Gly Ala Pro Met Glu Ser Asp Glu Gln Ala Gly
 275 280 285
 Ile Val Leu Ala Glu Asn Leu Ile His Asp Cys Thr Phe Ile Thr Ser
 290 295 300
 Glu Leu Thr Leu Ser His Ile Gly Val Trp Ala Ser Gly Glu Trp Glu
 305 310 315 320
 Cys Ser Val Ser Thr Val Gln Gly Asn Thr Ser Lys Lys Val Glu Ile
 325 330 335

Val Val Leu Glu Thr Ser Ala Ser Tyr Cys Pro Ala Glu Arg Val Thr
 340 345 350
 Asn Asn Arg Gly Asp Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr
 355 360 365
 Ala Tyr Gln Ser Cys Leu Gln Tyr Pro Phe Thr Ser Val Pro Leu Ser
 370 375 380
 Gly Gly Ala Pro Gly Thr Arg Ala Ser Arg Arg Cys Asp Arg Ala Gly
 385 390 395 400
 Arg Trp Glu Pro Gly Asp Tyr Ser His Cys Leu Tyr Thr Asn Asp Ile
 405 410 415
 Thr Arg Val Leu Tyr Thr Phe Val Leu Met Pro Ile Asn Ala Ser Asn
 420 425 430
 Ala Leu Thr Leu Ala His Gln Leu Arg Val Tyr Thr Ala Glu Ala Ala
 435 440 445
 Ser Phe Ser Asp Met Met Asp Val Val Tyr Val Ala Gln Met Ile Gln
 450 455 460
 Lys Phe Leu Gly Tyr Val Asp Gln Ile Lys Glu Leu Val Glu Val Met
 465 470 475 480
 Val Asp Met Ala Ser Asn Leu Met Leu Val Asp Glu His Leu Leu Trp
 485 490 495
 Leu Ala Gln Arg Glu Asp Lys Ala Cys Ser Gly Ile Val Gly Ala Leu
 500 505 510
 Glu Arg Ile Gly Gly Ala Ala Leu Ser Pro His Ala Gln His Ile Ser
 515 520 525
 Val Asn Ser Arg Asn Val Ala Leu Glu Ala Tyr Leu Ile Lys Pro His
 530 535 540
 Ser Tyr Val Gly Leu Thr Cys Thr Ala Phe Gln Arg Arg Glu Val Gly
 545 550 555 560
 Val Ser Gly Ala Gln Pro Ser Ser Val Gly Gln Asp Ala Pro Val Glu
 565 570 575
 Pro Glu Pro Leu Ala Asp Gln Gln Leu Arg Phe Arg Cys Thr Thr Gly
 580 585 590
 Arg Pro Asn Ile Ser Leu Ser Ser Phe His Ile Lys Asn Ser Val Ala
 595 600 605
 Leu Ala Ser Ile Gln Leu Pro Pro Ser Leu Phe Ser Thr Leu Pro Ala
 610 615 620
 Ala Leu Ala Pro Pro Val Pro Pro Asp Cys Thr Leu Gln Leu Leu Val
 625 630 635 640
 Phe Arg Asn Gly Arg Leu Phe Arg Ser His Gly Asn Asn Thr Ser Arg
 645 650 655
 Pro Gly Ala Ala Gly Pro Gly Lys Arg Arg Gly Val Ala Thr Pro Val
 660 665 670
 Ile Phe Ala Gly Thr Ser Gly Cys Gly Val Gly Asn Leu Thr Glu Pro
 675 680 685
 Val Ala Val Ser Leu Arg His Trp Ala Glu Gly Ala Asp Pro Met Ala
 690 695 700
 Ala Trp Trp Asn Gln Asp Gly Pro Gly Gly Trp Ser Ser Glu Gly Cys
 705 710 715 720
 Arg Leu Arg Tyr Ser Gln Pro Asn Val Ser Ser Leu Tyr Cys Gln His
 725 730 735
 Leu Gly Asn Val Ala Val Leu Met Glu Leu Asn Ala Phe Pro Arg Glu
 740 745 750
 Ala Gly Gly Ser Gly Ala Gly Leu His Pro Val Val Tyr Pro Cys Thr
 755 760 765
 Ala Leu Leu Leu Cys Leu Phe Ser Thr Ile Ile Thr Tyr Ile Leu
 770 775 780
 Asn His Ser Ser Ile His Val Ser Arg Lys Gly Trp His Met Leu Leu
 785 790 795 800
 Asn Leu Cys Phe His Met Ala Met Thr Ser Ala Val Phe Val Gly Gly
 805 810 815
 Val Thr Leu Thr Asn Tyr Gln Met Val Cys Gln Ala Val Gly Ile Thr

820	825	830
Leu His Tyr Ser Ser Leu Ser Ser	Leu Leu Trp Met Gly Val Lys Ala	
835	840	845
Arg Val Leu His Lys Glu Leu Ser Trp Arg Ala Pro Pro	Leu Glu Glu	
850	855	860
Gly Glu Ala Ala Pro Pro Gly Pro Arg Pro	Met Leu Arg Phe Tyr Leu	
865	870	875
Ile Ala Gly Gly Ile Pro Leu Ile Ile Cys Gly Ile Thr Ala Ala Val		880
885	890	895
Asn Ile His Asn Tyr Arg Asp His Ser Pro Tyr Cys Trp Leu Val Trp		
900	905	910
Arg Pro Ser Leu Gly Ala Phe Tyr Ile Pro Val Ala Leu Ile Leu Pro		
915	920	925
Ile Thr Trp Ile Tyr Phe Leu Cys Ala Gly Leu His Leu Arg Ser His		
930	935	940
Val Ala Gln Asn Pro Lys Gln Gly Asn Arg Ile Ser Leu, Glu Pro Gly		
945	950	955
Glu Glu Leu Arg Gly Ser Thr Arg Leu Arg Ser Ser Gly Val Leu Leu		960
965	970	975
Asn Asp Ser Gly Ser Leu Leu Ala Thr Val Ser Ala Gly Val Gly Thr		
980	985	990
Pro Ala Pro Pro Glu Asp Gly Asp Gly Val Tyr Ser Pro Gly Val Gln		
995	1000	1005
Leu Gly Ala Leu Met Thr Thr His Phe Leu Tyr Leu Ala Met Trp Ala		
1010	1015	1020
Cys Gly Ala Leu Ala Val Ser Gln Arg Trp Leu Pro Arg Val Val Cys		
1025	1030	1035
Ser Cys Leu Tyr Gly Val Ala Ala Ser Ala Leu Gly Leu Phe Val Phe		1040
1045	1050	1055
Thr His His Cys Ala Arg Arg Asp Val Arg Ala Ser Trp Arg Ala		
1060	1065	1070
Cys Cys Pro Pro Ala Ser Pro Ser Ala Ser His Val Pro Ala Arg Ala		
1075	1080	1085
Leu Pro Thr Ala Thr Glu Asp Gly Ser Pro Val Leu Gly Glu Gly Pro		
1090	1095	1100
Ala Ser Leu Lys Ser Ser Pro Ser Gly Ser Ser Gly Arg Ala Pro Pro		
1105	1110	1115
Pro Pro Cys Lys Leu Thr Asn Leu Gln Val Ala Gln Ser Gln Val Cys		1120
1125	1130	1135
Glu Ala Ser Val Ala Ala Arg Gly Asp Gly Glu Pro Glu Pro Thr Gly		
1140	1145	1150
Ser Arg Gly Ser Leu Ala Pro Arg His His Asn Asn Leu His His Gly		
1155	1160	1165
Arg Arg Val His Lys Ser Arg Ala Lys Gly His Arg Ala Gly Glu Thr		
1170	1175	1180
Gly Gly Lys Ser Arg Leu Lys Ala Leu Arg Ala Gly Thr Ser Pro Gly		
1185	1190	1195
Ala Pro Glu Leu Leu Ser Ser Glu Ser Gly Ser Leu His Asn Ser Pro		1200
1205	1210	1215
Ser Asp Ser Tyr Pro Gly Ser Ser Arg Asn Ser Pro Gly Asp Gly Leu		
1220	1225	1230
Pro Leu Glu Gly Glu Pro Met Leu Thr Pro Ser Glu Gly Ser Asp Thr		
1235	1240	1245
Ser Ala Ala Pro Ile Ala Glu Thr Gly Arg Pro Gly Gln Arg Arg Ser		
1250	1255	1260
Ala Ser Arg Asp Asn Leu Lys Gly Ser Gly Ser Ala Leu Glu Arg Glu		
1265	1270	1275
Ser Lys Arg Arg Ser Tyr Pro Leu Asn Thr Thr Ser Leu Asn Gly Ala		1280
1285	1290	1295
Pro Lys Gly Gly Lys Tyr Glu Asp Ala Ser Val Thr Gly Ala Glu Ala		
1300	1305	1310

Ile Ala Gly Gly Ser Met Lys Thr Gly Leu Trp Lys Ser Glu Thr Thr
 1315 1320 1325
 Val

<210> 192
<211> 500
<212> PRT
<213> Mus musculus

<400> 192
 Met Arg Ala Gln Leu Trp Leu Leu Gln Leu Leu Leu Arg Gly Ala
 1 5 10 15
 Ala Arg Ala Leu Ser Pro Ala Thr Pro Ala Gly His Asn Glu Gly Gln
 20 25 30
 Asp Ser Ala Trp Thr Ala Lys Arg Thr Arg Gln Gly Trp Ser Arg Arg
 35 40 45
 Pro Arg Glu Ser Pro Ala Gln Val Leu Lys Pro Gly Lys Thr Gln Leu
 50 55 60
 Ser Gln Asp Leu Gly Gly Ser Leu Ala Ile Asp Thr Leu Pro Asp
 65 70 75 80
 Asn Arg Thr Arg Val Val Glu Asp Asn His Asn Tyr Tyr Val Ser Arg
 85 90 95
 Val Tyr Gly Pro Gly Glu Lys Gln Ser Gln Asp Leu Trp Val Asp Leu
 100 105 110
 Ala Val Ala Asn Arg Ser His Val Lys Ile His Arg Ile Leu Ser Ser
 115 120 125
 Ser His Arg Gln Ala Ser Arg Val Val Leu Ser Phe Asp Phe Pro Phe
 130 135 140
 Tyr Gly His Pro Leu Arg Gln Ile Thr Ile Ala Thr Gly Gly Phe Ile
 145 150 155 160
 Phe Met Gly Asp Met Leu His Arg Met Leu Thr Ala Thr Gln Tyr Val
 165 170 175
 Ala Pro Leu Met Ala Asn Phe Asn Pro Gly Tyr Ser Asp Asn Ser Thr
 180 185 190
 Val Ala Tyr Phe Asp Asn Gly Thr Val Phe Val Val Gln Trp Asp His
 195 200 205
 Val Tyr Leu Gln Asp Arg Glu Asp Arg Gly Ser Phe Thr Phe Gln Ala
 210 215 220
 Ala Leu His Arg Asp Gly Arg Ile Val Phe Gly Tyr Lys Glu Ile Pro
 225 230 235 240
 Met Ala Val Leu Asp Ile Ser Ser Ala Gln His Pro Val Lys Ala Gly
 245 250 255
 Leu Ser Asp Ala Phe Met Ile Leu Asn Ser Ser Pro Glu Val Pro Glu
 260 265 270
 Ser Gln Arg Arg Thr Ile Phe Glu Tyr His Arg Val Glu Leu Asp Ser
 275 280 285
 Ser Lys Ile Thr Thr Ser Ala Val Glu Phe Thr Pro Leu Pro Thr
 290 295 300
 Cys Leu Gln His Gln Ser Cys Asp Thr Cys Val Ser Ser Asn Leu Thr
 305 310 315 320
 Phe Asn Cys Ser Trp Cys His Val Leu Gln Arg Cys Ser Ser Gly Phe
 325 330 335
 Asp Arg Tyr Arg Gln Glu Trp Leu Thr Tyr Gly Cys Ala Gln Glu Ala
 340 345 350
 Glu Gly Lys Thr Cys Glu Asp Phe Gln Asp Asp Ser His Tyr Ser Ala
 355 360 365
 Ser Pro Asp Ser Ser Phe Ser Pro Phe Asn Gly Asp Ser Thr Thr Ser
 370 375 380
 Ser Ser Leu Phe Ile Asp Ser Leu Thr Thr Glu Asp Asp Thr Lys Leu
 385 390 395 400

Asn Pro Tyr Ala Glu Gly Asp Gly Leu Pro Asp His Ser Ser Pro Lys
 405 410 415
 Ser Lys Gly Pro Pro Val His Leu Gly Thr Ile Val Gly Ile Val Leu
 420 425 430
 Ala Val Leu Leu Val Ala Ala Ile Ile Leu Ala Gly Ile Tyr Ile Ser
 435 440 445
 Gly His Pro Asn Ser Asn Ala Ala Leu Phe Phe Ile Glu Arg Arg Pro
 450 455 460
 His His Trp Pro Ala Met Lys Phe His Asn His Pro Asn His Ser Thr
 465 470 475 480
 Tyr Thr Glu Val Glu Pro Ser Gly His Glu Lys Glu Gly Phe Val Glu
 485 490 495
 Ala Glu Gln Cys
 500

<210> 193
 <211> 530
 <212> PRT
 <213> Mus musculus

<400> 193

Met Ala Arg Phe Arg Arg Ala Asp Leu Ala Ala Ala Gly Val Met Leu
 1 5 10 15
 Leu Cys His Phe Leu Thr Asp Arg Phe His Phe Ala His Gly Glu Pro
 20 25 30

Gly His His Thr Asn Asp Trp Ile Tyr Glu Val Thr Asn Ala Phe Pro
 35 40 45

Trp Asn Glu Glu Gly Val Glu Val Asp Ser Gln Ala Tyr Asn His Arg
 50 55 60

Trp Lys Arg Asn Val Asp Pro Phe Lys Ala Val Asp Thr Asn Arg Ala
 65 70 75 80

Ser Met Gly Gln Ala Ser Pro Glu Ser Lys Gly Phe Thr Asp Leu Leu
 85 90 95

Leu Asp Asp Gly Gln Asp Asn Asn Thr Gln Ile Glu Glu Asp Thr Asp
 100 105 110

His Asn Tyr Tyr Ile Ser Arg Ile Tyr Gly Pro Ala Asp Ser Ala Ser
 115 120 125

Arg Asp Leu Trp Val Asn Ile Asp Gln Met Glu Lys Asp Lys Val Lys
 130 135 140

Ile His Gly Ile Leu Ser Asn Thr His Arg Gln Ala Ala Arg Val Asn
 145 150 155 160

Leu Ser Phe Asp Phe Pro Phe Tyr Gly His Phe Leu Asn Glu Val Thr
 165 170 175

Val Ala Thr Gly Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met
 180 185 190

Leu Thr Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro
 195 200 205

Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala
 210 215 220

Leu Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu
 225 230 235 240

Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile
 245 250 255

Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr
 260 265 270

Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His
 275 280 285

Arg Ile Gln Gln Ile Pro Asn Val Arg Arg Arg Thr Ile Tyr Glu Tyr
 290 295 300

His Arg Val Glu Leu Gln Met Ser Lys Ile Thr Asn Ile Ser Ala Val
 305 310 315 320

Glu Met Thr Pro Leu Pro Thr Cys Leu Gln Phe Asn Gly Cys Gly Pro
 325 330 335
 Cys Val Ser Ser Gln Ile Gly Phe Asn Cys Ser Trp Cys Ser Lys Leu
 340 345 350
 Gln Arg Cys Ser Ser Gly Phe Asp Arg His Arg Gln Asp Trp Val Asp
 355 360 365
 Ser Gly Cys Pro Glu Glu Val Gln Ser Lys Glu Lys Met Cys Glu Lys
 370 375 380
 Thr Glu Pro Gly Glu Thr Ser Gln Thr Thr Thr Ser His Thr Thr
 385 390 395 400
 Thr Met Gln Phe Arg Val Leu Thr Thr Thr Arg Arg Ala Val Thr Ser
 405 410 415
 Gln Met Pro Thr Ser Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu
 420 425 430
 His Leu Lys Asp Ser Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys
 435 440 445
 Lys Gly Gly Thr Leu His Ala Gly Leu Ile Val Gly Ile Leu Ile Leu
 450 455 460
 Val Leu Ile Ile Ala Ala Ile Leu Val Thr Val Tyr Met Tyr His
 465 470 475 480
 His Pro Thr Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser
 485 490 495
 Arg Trp Pro Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala Tyr
 500 505 510
 Ala Glu Val Glu Pro Val Gly Glu Lys Glu Gly Phe Ile Val Ser Glu
 515 520 525
 Gln Cys
 530

<210> 194
 <211> 562
 <212> PRT
 <213> Mus musculus

<400> 194
 Met Asp Arg Ala Gly Arg Leu Gly Ala Gly Leu Arg Gly Leu Cys Val
 1 5 10 15
 Ala Ala Leu Val Leu Val Cys Ala Gly His Gly Gly Arg Arg Glu Asp
 20 25 30
 Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp
 35 40 45
 Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val
 50 55 60
 Glu Gln Leu Ala His Arg Phe Ile Ser Pro Gln Leu Arg Met Ser Phe
 65 70 75 80
 Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp
 85 90 95
 Arg Glu Gln Ile Arg Gln Gly Leu Glu Leu Gln Lys Val Leu Pro
 100 105 110
 Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln
 115 120 125
 Ile Tyr Tyr Glu Asn Ser Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile
 130 135 140
 Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu
 145 150 155 160
 Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val
 165 170 175
 Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser
 180 185 190
 Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly
 195 200 205

Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala
 210 215 220
 Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg
 225 230 235 240
 Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser
 245 250 255
 Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Pro Phe Ala Val
 260 265 270
 Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly
 275 280 285
 Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile
 290 295 300
 Ser Ser Ser Val Ile Ile Thr Thr His Cys Ser Asp Gly Ser Ile
 305 310 315 320
 Leu Ala Ile Ala Leu Leu Val Leu Phe Leu Leu Ala Leu Ala Leu
 325 330 335
 Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys Glu Val
 340 345 350
 Pro Pro Pro Pro Val Glu Glu Ser Glu Glu Asp Asp Asp Gly Leu
 355 360 365
 Pro Lys Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly Gly Arg
 370 375 380
 Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu Lys Gly
 385 390 395 400
 Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala Arg Val
 405 410 415
 Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn Leu Asn
 420 425 430
 Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser Pro Ile
 435 440 445
 Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly Tyr Asp
 450 455 460
 Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg Cys Ile
 465 470 475 480
 Asn Phe Thr Arg Val Lys Asn Ser Gln Pro Ala Lys Tyr Pro Leu Asn
 485 490 495
 Asn Thr Tyr His Pro Ser Ser Pro Pro Ala Pro Ile Tyr Thr Pro
 500 505 510
 Pro Pro Pro Ala Pro His Cys Pro Pro Pro Ala Pro Ser Ala Pro Thr
 515 520 525
 Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro Gln Ala
 530 535 540
 Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro Arg Pro
 545 550 555 560
 Ser Val

<210> 195
 <211> 2565
 <212> DNA
 <213> Homo sapiens

<400> 195

tcgcgatgt	gctgcgcctg	ttgctggcct	ggggggccgc	agggcccaca	ctggggccagg	60
accctgggc	tgctgagccc	cgtgccgcct	ggggccccag	cagctgctac	gctcttcc	120
cacggcgccg	cacettcccg	gaggcctggc	gggcctggc	cgagctgggg	ggcacctgg	180
ccactcctcg	gaccggccag	gaggcccagc	gtgtggacag	cctgggtgggt	gcgggcccag	240
ccagggcggt	gctgtggat	gggcgtgcagc	ggcaggcccg	gcaatgccag	ctgcagcgcc	300
cactgcgcgg	tttcacgtgg	accacagggg	accaggacac	ggctttcacc	aactggggcc	360
agccagcctc	tggaggcccc	tgcggccccc	agcgctgtgt	ggccctggag	gcaagtggcg	420
agcaccgctg	gctggagggc	tcgtcacgc	tggctgtcga	cggctacctg	tgccagtttgc	480

gcttcgaggg	cgccctgccc	gcgctgcaag	atgaggcggg	ccaggccggc	ccagccgtgt
ataccacgcc	cttccacctg	gtctccacag	agtttgagtg	gctgcccttc	ggctctgtgg
ccgctgtgca	gtgccaggct	ggcaggggag	cctctctgct	ctgcgtgaag	cagcctgagg
gaggtgtggg	ctggcacgg	gctggggccc	tgtgcctggg	gactggctgc	agccctgaca
acgggggctg	cgaacacgaa	tgtgtggagg	aggtggatgg	tcacgtgtcc	tggcgtgcga
ctgagggctt	ccggctggca	gcagacgggc	gcagttgcga	ggaccctgt	gcccaggctc
cgtgcgagca	gcagtgtgag	cccggggc	cacaaggcta	cagctccac	tgtcgcctgg
gtttccggcc	agcggaggat	gatccgcacc	gctgtgtgga	cacagatgag	tgccagattg
ccggtgtgtg	ccagcagatg	tgtgtcaact	acgttggtgg	cttcgagtgt	tatttagcgt
agggacatga	gctggaggct	gatggcatca	gctgcagccc	tgcagggggcc	atgggtgccc
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<210> 196
<211> 757
<212> PRT
<213> *Homo sapiens*

<400> 196
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 35 40 45
 Arg Ala Cys Arg Glu Leu Gly Gly Asp Leu Ala Thr Pro Arg Thr Pro
 50 55 60
 Glu Glu Ala Gln Arg Val Asp Ser Leu Val Gly Ala Gly Pro Ala Ser
 65 70 75 80
 Arg Leu Leu Trp Ile Gly Leu Gln Arg Gln Ala Arg Gln Cys Gln Leu
 85 90 95
 Gln Arg Pro Leu Arg Gly Phe Thr Trp Thr Thr Gly Asp Gln Asp Thr
 100 105 110
 Ala Phe Thr Asn Trp Ala Gln Pro Ala Ser Gly Gly Pro Cys Pro Ala
 115 120 125
 Gln Arg Cys Val Ala Leu Glu Ala Ser Gly Glu His Arg Trp Leu Glu
 130 135 140
 Gly Ser Cys Thr Leu Ala Val Asp Gly Tyr Leu Cys Gln Phe Gly Phe

145	150	155	160												
Glu	Gly	Ala	Cys	Pro	Ala	Leu	Gln	Asp	Glu	Ala	Gly	Gln	Ala	Gly	Pro
165									170						175
Ala	Val	Tyr	Thr	Thr	Pro	Phe	His	Leu	Val	Ser	Thr	Glu	Phe	Glu	Trp
180									185						190
Leu	Pro	Phe	Gly	Ser	Val	Ala	Ala	Val	Gln	Cys	Gln	Ala	Gly	Arg	Gly
195									200					205	
Ala	Ser	Leu	Leu	Cys	Val	Lys	Gln	Pro	Glu	Gly	Gly	Val	Gly	Trp	Ser
210						215						220			
Arg	Ala	Gly	Pro	Leu	Cys	Leu	Gly	Thr	Gly	Cys	Ser	Pro	Asp	Asn	Gly
225						230				235					240
Gly	Cys	Glu	His	Glu	Cys	Val	Glu	Glu	Val	Asp	Gly	His	Val	Ser	Cys
									245		250				255
Arg	Cys	Thr	Glu	Gly	Phe	Arg	Leu	Ala	Ala	Asp	Gly	Arg	Ser	Cys	Glu
			260			265						270			
Asp	Pro	Cys	Ala	Gln	Ala	Pro	Cys	Glu	Gln	Gln	Cys	Glu	Pro	Gly	Gly
			275			280						285			
Pro	Gln	Gly	Tyr	Ser	Cys	His	Cys	Arg	Leu	Gly	Phe	Arg	Pro	Ala	Glu
			290			295					300				
Asp	Asp	Pro	His	Arg	Cys	Val	Asp	Thr	Asp	Glu	Cys	Gln	Ile	Ala	Gly
			305			310					315				320
Val	Cys	Gln	Gln	Met	Cys	Val	Asn	Tyr	Val	Gly	Gly	Phe	Glu	Cys	Tyr
									325		330				335
Cys	Ser	Glu	Gly	His	Glu	Leu	Glu	Ala	Asp	Gly	Ile	Ser	Cys	Ser	Pro
						340				345					350
Ala	Gly	Ala	Met	Gly	Ala	Gln	Ala	Ser	Gln	Asp	Leu	Gly	Asp	Glu	Leu
						355			360			365			
Leu	Asp	Asp	Gly	Glu	Asp	Glu	Glu	Asp	Glu	Asp	Glu	Ala	Trp	Lys	Ala
			370			375						380			
Phe	Asn	Gly	Gly	Trp	Thr	Glu	Met	Pro	Gly	Ile	Leu	Trp	Met	Glu	Pro
			385			390					395				400
Thr	Gln	Pro	Pro	Asp	Phe	Ala	Leu	Ala	Tyr	Arg	Pro	Ser	Phe	Pro	Glu
						405				410					415
Asp	Arg	Glu	Pro	Gln	Ile	Pro	Tyr	Pro	Glu	Pro	Thr	Trp	Pro	Pro	Pro
			420			425									430
Leu	Ser	Ala	Pro	Arg	Val	Pro	Tyr	His	Ser	Ser	Val	Leu	Ser	Val	Thr
						435			440			445			
Arg	Pro	Val	Val	Val	Ser	Ala	Thr	His	Pro	Thr	Leu	Pro	Ser	Ala	His
						450			455			460			
Gln	Pro	Pro	Val	Ile	Pro	Ala	Thr	His	Pro	Ala	Leu	Ser	Arg	Asp	His
			465			470					475				480
Gln	Ile	Pro	Val	Ile	Ala	Ala	Asn	Tyr	Pro	Asp	Leu	Pro	Ser	Ala	Tyr
						485					490				495
Gln	Pro	Gly	Ile	Leu	Ser	Val	Ser	His	Ser	Ala	Gln	Pro	Pro	Ala	His
				500					505						510
Gln	Pro	Pro	Met	Ile	Ser	Thr	Lys	Tyr	Pro	Glu	Leu	Phe	Pro	Ala	His
			515			520					525				
Gln	Ser	Pro	Met	Phe	Pro	Asp	Thr	Arg	Val	Ala	Gly	Thr	Gln	Thr	Thr
			530			535					540				
Thr	His	Leu	Pro	Gly	Ile	Pro	Pro	Asn	His	Ala	Pro	Leu	Val	Thr	Thr
			545			550					555				560
Leu	Gly	Ala	Gln	Leu	Pro	Pro	Gln	Ala	Pro	Asp	Ala	Leu	Val	Leu	Arg
						565				570					575
Thr	Gln	Ala	Thr	Gln	Leu	Pro	Ile	Ile	Pro	Thr	Ala	Gln	Pro	Ser	Leu
						580			585			590			
Thr	Thr	Thr	Ser	Arg	Ser	Pro	Val	Ser	Pro	Ala	His	Gln	Ile	Ser	Val
						595			600			605			
Pro	Ala	Ala	Thr	Gln	Pro	Ala	Ala	Leu	Pro	Thr	Leu	Leu	Pro	Ser	Gln
			610			615						620			
Ser	Pro	Thr	Asn	Gln	Thr	Ser	Pro	Ile	Ser	Pro	Thr	His	Pro	His	Ser
			625			630					635				640

Lys Ala Pro Gln Ile Pro Arg Glu Asp Gly Pro Ser Pro Lys Leu Ala
 645 650 655
 Leu Trp Leu Pro Ser Pro Ala Pro Thr Ala Ala Pro Thr Ala Leu Gly
 660 665 670
 Glu Ala Gly Leu Ala Glu His Ser Gln Arg Asp Asp Arg Trp Leu Leu
 675 680 685
 Val Ala Leu Leu Val Pro Thr Cys Val Phe Leu Val Val Leu Leu Ala
 690 695 700
 Leu Gly Ile Val Tyr Cys Thr Arg Cys Gly Pro His Ala Pro Asn Lys
 705 710 715 720
 Arg Ile Thr Asp Cys Tyr Arg Trp Val Ile His Ala Gly Ser Lys Ser
 725 730 735
 Pro Thr Glu Pro Met Pro Pro Arg Gly Ser Leu Thr Gly Val Gln Thr
 740 745 750
 Cys Arg Thr Ser Val
 755

<210> 197
<211> 2973
<212> DNA
<213> Homo sapiens

<400> 197

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gcaggcagct	ccccgcagct	ccggcgctt	ccaggcagct	ctctgagcc	tgccagaggc	180
ccggccgc	atccccagcc	ccgagccatg	atgaagac	ttgtccagcg	gaactgcacg	240
ctcagtgtgc	ccgc	aaaaaa	ctcataccgc	atgtgtgtc	tgggtgc	300
aagagctcca	tcgtgtctcg	cttc	cttcaat	ggccg	tttgg	360
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ttccacccca	ggcc	cttgc	cat	gccc	gcgc	900
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cacagctct	tgg	tgtt	atc	gg	catctgc	1260
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cacagaaggc	ca	gat	ggaa	gg	tttgc	1440
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tctgcacccc	ct	cc	ccac	cc	tttgc	1560
gagccagtgg	act	ctgt	tgaa	gg	tttgc	1620
cttagaccac	g	cc	ccac	cc	tttgc	1680
cgacagttgt	gtt	ttgt	gttgc	gg	tttgc	1740
gaaatcattg	tac	tttt	actgt	tttgc	tttgc	1800
agatccacgg	c	cc	ccac	cc	tttgc	1860
cctgtttgca	g	cc	ccac	cc	tttgc	1920
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<210> 198
<211> 266
<212> PRT
<213> Homo sapiens

<400> 198															
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			20					25					30		
Ser	Ser	Ile	Val	Ser	Arg	Phe	Leu	Asn	Gly	Arg	Phe	Glu	Asp	Gln	Tyr
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Thr	Pro	Thr	Ile	Glu	Asp	Phe	His	Arg	Lys	Val	Tyr	Asn	Ile	Arg	Gly
		50					55				60				
Asp	Met	Tyr	Gln	Leu	Asp	Ile	Leu	Asp	Thr	Ser	Gly	Asn	His	Pro	Phe
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Pro	Ala	Met	Arg	Arg	Leu	Ser	Ile	Leu	Thr	Gly	Asp	Val	Phe	Ile	Leu
							85			90			95		
Val	Phe	Ser	Leu	Asp	Asn	Arg	Glu	Ser	Phe	Asp	Glu	Val	Lys	Arg	Leu
			100					105					110		
Gln	Lys	Gln	Ile	Leu	Glu	Val	Lys	Ser	Cys	Leu	Lys	Asn	Lys	Thr	Lys
		115						120					125		
Glu	Ala	Ala	Glu	Leu	Pro	Met	Val	Ile	Cys	Gly	Asn	Lys	Asn	Asp	His
		130						135			140				
Gly	Glu	Leu	Cys	Arg	Gln	Val	Pro	Thr	Thr	Glu	Ala	Glu	Leu	Leu	Val
	145						150			155			160		
Ser	Gly	Asp	Glu	Asn	Cys	Ala	Tyr	Phe	Glu	Val	Ser	Ala	Lys	Lys	Asn
			165					170					175		
Thr	Asn	Val	Asp	Glu	Met	Phe	Tyr	Val	Leu	Phe	Ser	Met	Ala	Lys	Leu
		180					185						190		
Pro	His	Glu	Met	Ser	Pro	Ala	Leu	His	Arg	Lys	Ile	Ser	Val	Gln	Tyr
		195					200						205		
Gly	Asp	Ala	Phe	His	Pro	Arg	Pro	Phe	Cys	Met	Arg	Arg	Val	Lys	Glu
		210					215						220		
Met	Asp	Ala	Tyr	Gly	Met	Val	Ser	Pro	Phe	Ala	Arg	Arg	Pro	Ser	Val
	225						230				235			240	
Asn	Ser	Asp	Leu	Lys	Tyr	Ile	Lys	Ala	Lys	Val	Leu	Arg	Glu	Gly	Gln
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Ala	Arg	Glu	Arg	Asp	Lys	Cys	Thr	Ile	Gln						
		260						265							

<210> 199
<211> 2159
<212> DNA
<213> Homo sapiens

<400> 199
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gattggcagt atggagttac tcagcccttc cctcacacag aggaggaggt ggaagtttat	180
tcacacgcgt acagccacag gtggaaaaga aacttggact ttctcaaggc ggttagacacg	240
aaccgagcaa gcgtcgccca agactctctt gagcccagaa gcttcacaga cctgctgt	300
gatgatgggc aggacaataa cactcagatc gaggaggata cagaccacaa ttactatata	360
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agaagaacaa ttatgaata ccaccggata gagctacaaa tgtcaaaaat taccaacatt	960
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ggatttgate gtcatcgca ggactgggtg gacagtggat gcccgtgaaga gtcaaaagag	1140
aagatgtgtg agaatacaga accagtggaa acttcttcga gaaccaccac aaccatagga	1200
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gttggaatcc tcatcctgtt cctcattgtt ggcacagcca ttcttgcgatc agtctatatg	1440
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ttcaaatgtt ctctgtatgc tcaaagataa ctgttttcca aagcctgaac cctttactc	1920
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	2100
	2159

<210> 200
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 200
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 Gly Asp Gln Ile Leu Asp Trp Gln Tyr Gly Val Thr Gln Ala Phe Pro
 35 40 45
 His Thr Glu Glu Glu Val Glu Val Asp Ser His Ala Tyr Ser His Arg
 50 55 60
 Trp Lys Arg Asn Leu Asp Phe Leu Lys Ala Val Asp Thr Asn Arg Ala
 65 70 75 80
 Ser Val Gly Gln Asp Ser Pro Glu Pro Arg Ser Phe Thr Asp Leu Leu
 85 90 95
 Leu Asp Asp Gly Gln Asp Asn Asn Thr Gln Ile Glu Glu Asp Thr Asp
 100 105 110
 His Asn Tyr Tyr Ile Ser Arg Ile Tyr Gly Pro Ser Asp Ser Ala Ser
 115 120 125
 Arg Asp Leu Trp Val Asn Ile Asp Gln Met Glu Lys Asp Lys Val Lys
 130 135 140
 Ile His Gly Ile Leu Ser Asn Thr His Arg Gln Ala Ala Arg Val Asn

145	150	155	160
Leu Ser Phe Asp Phe Pro Phe Tyr Gly His	Phe Leu Arg Glu Ile Thr		
165	170	175	
Val Ala Thr Gly Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met			
180	185	190	
Leu Thr Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro			
195	200	205	
Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala			
210	215	220	
Leu Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu			
225	230	235	240
Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile			
245	250	255	
Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr			
260	265	270	
Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His			
275	280	285	
Arg Ile Gln Gln Ile Pro Asn Val Arg Arg Arg Thr Ile Tyr Glu Tyr			
290	295	300	
His Arg Val Glu Leu Gln Met Ser Lys Ile Thr Asn Ile Ser Ala Val			
305	310	315	320
Glu Met Thr Pro Leu Pro Thr Cys Leu Gln Phe Asn Arg Cys Gly Pro			
325	330	335	
Cys Val Ser Ser Gln Ile Gly Phe Asn Cys Ser Trp Cys Ser Lys Leu			
340	345	350	
Gln Arg Cys Ser Ser Gly Phe Asp Arg His Arg Gln Asp Trp Val Asp			
355	360	365	
Ser Gly Cys Pro Glu Glu Ser Lys Glu Lys Met Cys Glu Asn Thr Glu			
370	375	380	
Pro Val Glu Thr Ser Ser Arg Thr Thr Thr Thr Ile Gly Ala Thr Thr			
385	390	395	400
Thr Gln Phe Arg Val Leu Thr Thr Thr Arg Arg Ala Val Thr Ser Gln			
405	410	415	
Phe Pro Thr Ser Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu His			
420	425	430	
Leu Lys Asp Asn Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys Lys			
435	440	445	
Gly Gly Thr Leu His Ala Gly Leu Ile Val Gly Ile Leu Ile Leu Val			
450	455	460	
Leu Ile Val Ala Thr Ala Ile Leu Val Thr Val Tyr Met Tyr His His			
465	470	475	480
Pro Thr Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser Arg			
485	490	495	
Trp Pro Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala Tyr Ala			
500	505	510	
Glu Val Glu Pro Val Gly Glu Lys Glu Gly Phe Ile Val Ser Glu Gln			
515	520	525	
Cys			

<210> 201
 <211> 2608
 <212> DNA
 <213> Homo sapiens

<400> 201

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<211> 350

<212> PRT

<213> Homo sapiens

<400> 202

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<212> DNA

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 Arg Ser Pro Ser Phe Gly Ala Gly Glu Gly Leu Leu Arg Ser Gln Ala
 420 425 430
 Arg Thr Arg Ala Lys Gly Pro Gly Gly Thr Ser Arg Ala Leu Arg Asp
 435 440 445
 Gly Gly Phe Glu Pro Glu Lys Ser Arg Gln Arg Lys Ser Leu Ser Asn
 450 455 460
 Pro Asp Ile Ala Ser Glu Thr Leu Thr Leu Ser Phe Leu Arg Ser
 465 470 475 480
 Asp Leu Ser Glu Leu Arg Val Arg Lys Pro Gly Gly Ser Ser Gly Asp
 485 490 495
 Arg Gly Ser Asn Pro Leu Asp Gly Arg Asp Ser Pro Ser Ala Gly Gly
 500 505 510
 Pro Val Gly Gln Leu Glu Pro Ile Pro Ile Pro Ala Pro Ala Ser Pro
 515 520 525
 Gly Thr Arg Pro Thr Leu Lys Asp Leu Thr Ala Thr Leu Arg Arg Ala
 530 535 540
 Lys Ser Phe Thr Cys Ser Glu Lys Pro Met Ala Arg Arg Leu Pro Arg
 545 550 555 560
 Thr Ser Ala Leu Lys Ser Ser Ser Ser Glu Leu Leu Leu Thr Gly Pro
 565 570 575
 Gly Ala Glu Glu Asp Pro Leu Pro Leu Ile Val Gln Asp Gln Tyr Val

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Gln	Glu	Ala	Arg	Gln	Val	Phe	Glu	Lys	Ile	Gln	Arg	Met	Gly	Ala	Gln
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Gln	Asp	Asp	Gly	Ser	Asp	Ala	Pro	Pro	Gly	Ser	Pro	Asp	Trp	Ala	Gly
	610				615					620					
Asp	Val	Thr	Arg	Gly	Gln	Arg	Ser	Gln	Glu	Leu	Ser	Gly	Pro	Glu	
	625				630					635				640	
Ser	Ser	Leu	Thr	Asp	Gly	Ile	Gly	Ala	Asp	Pro	Glu	Pro	Pro	Val	
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Ala	Ala	Phe	Cys	Gly	Leu	Gly	Thr	Thr	Gly	Met	Trp	Arg	Pro	Leu	Ser
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Ser	Ser	Ser	Ala	Gln	Thr	Asn	His	His	Gly	Pro	Gly	Thr	Glu	Asp	Ser
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Leu	Gly	Gly	Trp	Ala	Leu	Val	Ser	Pro	Glu	Thr	Pro	Pro	Thr	Pro	Gly
	690				695					700					
Ala	Leu	Arg	Arg	Arg	Arg	Lys	Val	Pro	Pro	Ser	Gly	Ser	Gly	Ser	
	705				710					715				720	
Glu	Leu	Ser	Asn	Gly	Glu	Ala	Gly	Glu	Ala	Tyr	Arg	Ser	Leu	Ser	Asp
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Pro	Ile	Pro	Gln	Arg	His	Arg	Ala	Ala	Thr	Ser	Glu	Glu	Pro	Thr	Gly
					740					745				750	
Phe	Ser	Val	Asp	Ser	Asn	Leu	Leu	Gly	Ser	Leu	Ser	Pro	Lys	Thr	Gly
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Leu	Pro	Ala	Thr	Ser	Ala	Met	Asp	Glu	Gly	Leu	Thr	Ser	Gly	His	Ser
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Asp	Trp	Ser	Val	Gly	Ser	Glu	Glu	Ser	Lys	Gly	Tyr	Gln	Glu	Val	Ile
	785				790					795				800	
Gln	Ser	Ile	Val	Gln	Gly	Pro	Gly	Thr	Leu	Gly	Arg	Val	Val	Asp	Asp
					805					810				815	
Arg	Ile	Ala	Gly	Lys	Ala	Pro	Lys	Lys	Ser	Leu	Ser	Asp	Pro	Ser	
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Arg	Arg	Gly	Glu	Leu	Ala	Gly	Pro	Gly	Phe	Glu	Gly	Pro	Gly	Gly	Glu
					835					840				845	
Pro	Ile	Arg	Glu	Val	Glu	Pro	Met	Leu	Pro	Pro	Ser	Ser	Ser	Glu	Pro
					850					855				860	
Ile	Leu	Val	Glu	Gln	Arg	Ala	Glu	Pro	Glu	Glu	Pro	Gly	Ala	Thr	Arg
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Ser	Arg	Ala	Gln	Ser	Glu	Arg	Ala	Leu	Pro	Glu	Ala	Leu	Pro	Pro	Pro
					885					890				895	
Ala	Thr	Ala	His	Arg	Asn	Phe	His	Leu	Asp	Pro	Lys	Leu	Ala	Asp	Ile
					900					905				910	
Leu	Ser	Pro	Arg	Leu	Ile	Arg	Arg	Gly	Ser	Lys	Lys	Arg	Pro	Ala	Arg
					915					920				925	
Ser	Ser	His	Gln	Glu	Leu	Arg	Arg	Asp	Glu	Gly	Ser	Gln	Asp	Gln	Thr
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Gly	Ser	Leu	Ser	Arg	Ala	Arg	Pro	Ser	Ser	Arg	His	Val	Arg	His	Ala
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Ser	Val	Pro	Ala	Thr	Phe	Met	Pro	Ile	Val	Val	Pro	Glu	Pro	Pro	Thr
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Ser	Val	Gly	Pro	Pro	Val	Ala	Val	Pro	Glu	Ile	Gly	Phe	Pro	Thr	
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Arg	Ala	His	Pro	Thr	Leu	Gln	Ala	Pro	Ser	Leu	Glu	Asp	Val	Thr	Lys
					995					1000				1005	
Gln	Tyr	Met	Leu	Asn	Leu	His	Ser	Gly	Glu	Val	Pro	Ala	Pro	Val	Pro
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Val	Asp	Met	Pro	Cys	Leu	Pro	Leu	Ala	Ala	Pro	Pro	Ser	Ala	Glu	Ala
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Lys	Pro	Pro	Glu	Ala	Ala	Arg	Pro	Ala	Asp	Glu	Pro	Thr	Pro	Ala	Ser
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Lys	Cys	Cys	Ser	Lys	Pro	Gln	Val	Asp	Met	Arg	Lys	His	Val	Ala	Met
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 Met Gln Gly Tyr Met Gln Pro Leu Lys Gln Pro Glu Asn Ser Val Leu
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 Cys Asp Pro Ser Leu Val Asp Glu Ile Phe Asp Gln Ile Pro Glu Leu
 1105 1110 1115 1120
 Leu Glu His His Glu Gln Phe Leu Glu Gln Val Arg His Cys Met Gln
 1125 1130 1135
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 Ser Lys Asp Val Leu Val Asn Ile Tyr Ser Ala Tyr Ile Asp Asn Phe
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 1170 1175 1180
 Phe Leu Lys Phe Leu Glu Gln Ser Met Arg Glu Asn Lys Glu Lys Gln
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 Ala Leu Ser Asp Leu Met Ile Lys Pro Val Gln Arg Ile Pro Arg Tyr
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 Glu Leu Leu Val Lys Asp Leu Leu Lys His Thr Pro Glu Asp His Pro
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 Asp His Pro Leu Leu Leu Glu Ala Gln Arg Asn Ile Lys Gln Val Ala
 1235 1240 1245
 Glu Arg Ile Asn Lys Gly Val Arg Ser Ala Glu Glu Ala Glu Arg His
 1250 1255 1260
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 1265 1270 1275 1280
 Leu Gln Ala Pro Leu Arg Arg Phe Leu Arg Gln Glu Met Val Ile Glu
 1285 1290 1295
 Val Lys Ala Ile Gly Gly Lys Asp Arg Ser Leu Phe Leu Phe Thr
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 Asp Leu Ile Val Cys Thr Thr Leu Lys Arg Lys Ser Gly Ser Leu Arg
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 Arg Ser Ser Met Ser Leu Tyr Thr Ala Ala Ser Val Ile Asp Thr Ala
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 Ser Lys Tyr Lys Met Leu Trp Lys Leu Pro Leu Glu Asp Ala Asp Ile
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 Ile Lys Gly Ala Ser Gln Ala Thr Asn Arg Glu Asn Ile Gln Lys Ala
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 Ile Ser Arg Leu Asp Glu Asp Leu Thr Thr Leu Gly Gln Met Ser Lys
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 Leu Ser Glu Ser Leu Gly Phe Pro His Gln Ser Leu Asp Asp Ala Leu
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 Leu Cys Tyr Ala Leu Ser Phe Pro Pro Thr Lys Leu Glu Leu Cys Ala
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 Thr Arg Pro Glu Gly Thr Asp Ser Tyr Ile Phe Glu Phe Pro His Pro
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 Asp Ala Arg Leu Gly Phe Glu Gln Ala Phe Asp Glu Ala Lys Arg Lys
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 Leu Ala Ser Ser Lys Ser Cys Leu Asp Pro Glu Phe Leu Lys Ala Ile
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 Pro Ile Met Lys Thr Arg Ser Gly Met Gln Phe Ser Cys Ala Ala Pro
 1490 1495 1500
 Thr Leu Asn Ser Cys Pro Glu Pro Ser Pro Glu Val Trp Val Cys Asn
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 Ser Asp Gly Tyr Val Gly Gln Val Cys Leu Leu Ser Leu Arg Ala Glu
 1525 1530 1535
 Pro Asp Val Glu Ala Cys Ile Ala Val Cys Ser Ala Arg Ile Leu Cys
 1540 1545 1550
 Ile Gly Ala Val Pro Gly Leu Gln Pro Arg Cys His Arg Glu Pro Pro

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Pro Ser Leu Arg Ser Pro Pro Glu Thr Ala Pro Glu Pro Ala Gly Pro		
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Glu Leu Asp Val Glu Ala Ala Ala Asp Glu Glu Ala Ala Thr Leu Ala		
1585	1590	1595
Glu Pro Gly Pro Gln Pro Cys Leu His Ile Ser Ile Ala Gly Ser Gly		
1605	1610	1615
Leu Glu Met Thr Pro Gly Leu Gly Glu Gly Asp Pro Arg Pro Glu Leu		
1620	1625	1630
Val Pro Phe Asp Ser Asp Ser Asp Asp Glu Ser Ser Pro Ser Pro Ser		
1635	1640	1645
Gly Thr Leu Gln Ser Gln Ala Ser Arg Ser Thr Ile Ser Ser Ser Phe		
1650	1655	1660
Gly Asn Glu Glu Thr Pro Ser Ser Lys Glu Ala Thr Ala Glu Thr Thr		
1665	1670	1675
Ser Ser Glu Glu Gln Glu Pro Gly Phe Leu Pro Leu Ser Gly Ser		
1685	1690	1695
Phe Gly Pro Gly Gly Pro Cys Gly Thr Ser Pro Met Asp Gly Arg Ala		
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Leu Arg Arg Ser Ser His Gly Ser Phe Thr Arg Gly Ser Leu Glu Asp		
1715	1720	1725
Leu Leu Ser Val Asp Pro Glu Ala Tyr Gln Ser Ser Val Trp Leu Gly		
1730	1735	1740
Thr Glu Asp Gly Cys Val His Val Tyr Gln Ser Ser Asp Ser Ile Arg		
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Asp Arg Arg Asn Ser Met Lys Leu Gln His Ala Ala Ser Val Thr Cys		
1765	1770	1775
Ile Leu Tyr Leu Asn Asn Gln Val Phe Val Ser Leu Ala Asn Gly Glu		
1780	1785	1790
Leu Val Val Tyr Gln Arg Glu Ala Gly His Phe Trp Asp Pro Gln Asn		
1795	1800	1805
Phe Lys Ser Val Thr Leu Gly Thr Gln Gly Ser Pro Ile Thr Lys Met		
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Val Ser Val Gly Gly Arg Leu Trp Cys Gly Cys Gln Asn Arg Val Leu		
1825	1830	1835
Val Leu Ser Pro Asp Thr Leu Gln Leu Glu His Met Phe Tyr Val Gly		
1845	1850	1855
Gln Asp Ser Ser Arg Cys Val Ala Cys Met Val Asp Ser Ser Leu Gly		
1860	1865	1870
Val Trp Val Thr Leu Lys Gly Ser Ala His Val Cys Leu Tyr His Pro		
1875	1880	1885
Asp Thr Phe Glu Gln Leu Ala Glu Val Asp Val Thr Pro Pro Val His		
1890	1895	1900
Arg Met Leu Ala Gly Ser Asp Ala Ile Ile Arg Gln His Lys Ala Ala		
1905	1910	1915
Cys Leu Arg Ile Thr Ala Leu Leu Val Cys Glu Glu Leu Leu Trp Val		
1925	1930	1935
Gly Thr Ser Ala Gly Val Val Leu Thr Met Pro Thr Ser Pro Gly Thr		
1940	1945	1950
Val Ser Cys Pro Arg Ala Pro Leu Ser Pro Thr Gly Leu Gly Gln Gly		
1955	1960	1965
His Thr Gly His Val Arg Phe Leu Ala Ala Val Gln Leu Pro Asp Gly		
1970	1975	1980
Phe Asn Leu Leu Cys Pro Thr Pro Pro Pro Pro Asp Thr Gly Pro		
1985	1990	1995
Glu Lys Leu Pro Ser Leu Glu His Arg Asp Ser Pro Trp His Arg Gly		
2005	2010	2015
Pro Ala Pro Ala Arg Pro Lys Met Leu Val Ile Ser Gly Gly Asp Gly		
2020	2025	2030
Tyr Glu Asp Phe Arg Leu Ser Ser Gly Gly Ser Ser Ser Glu Thr		
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Val Gly Arg Asp Asp Ser Thr Asn His Leu Leu Leu Trp Arg Val
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<210> 205
<211> 2247
<212> DNA
<213> Homo sapiens

<400> 205

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<210> 206
<211> 488
<212> PRT
<213> Homo sapiens

<400> 206

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Pro Pro Met Leu Leu Leu Leu Gln Pro Pro Pro Leu Leu Ala Arg			
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Ala Leu Pro Pro Asp Val His His Leu His Ala Glu Arg Arg Gly Pro			
35	40	45	
Gln Pro Trp His Ala Ala Leu Pro Ser Ser Pro Ala Pro Ala Pro Ala			

50	55	60
Thr Gln Glu Ala Pro Arg Pro Ala Ser Ser	Leu Arg Pro Pro Arg Cys	
65	70	75
Gly Val Pro Asp Pro Ser Asp Gly Leu Ser Ala Arg Asn Arg Gln Lys		80
85	90	95
Arg Phe Val Leu Ser Gly Gly Arg Trp Glu Lys Thr Asp Leu Thr Tyr		
100	105	110
Arg Ile Leu Arg Phe Pro Trp Gln Leu Val Gln Glu Gln Val Arg Gln		
115	120	125
Thr Met Ala Glu Ala Leu Lys Val Trp Ser Asp Val Thr Pro Leu Thr		
130	135	140
Phe Thr Glu Val His Glu Gly Arg Ala Asp Ile Met Ile Asp Phe Ala		
145	150	155
Arg Tyr Trp His Gly Asp Asp Leu Pro Phe Asp Gly Pro Gly Gly Ile		160
165	170	175
Leu Ala His Ala Phe Pro Lys Thr His Arg Glu Gly Asp Val His		
180	185	190
Phe Asp Tyr Asp Glu Thr Trp Thr Ile Gly Asp Asp Gln Gly Thr Asp		
195	200	205
Leu Leu Gln Val Ala Ala His Glu Phe Gly His Val Leu Gly Leu Gln		
210	215	220
His Thr Thr Ala Ala Lys Ala Leu Met Ser Ala Phe Tyr Thr Phe Arg		
225	230	235
Tyr Pro Leu Ser Leu Ser Pro Asp Asp Cys Arg Gly Val Gln His Leu		240
245	250	255
Tyr Gly Gln Pro Trp Pro Thr Val Thr Ser Arg Thr Pro Ala Leu Gly		
260	265	270
Pro Gln Ala Gly Ile Asp Thr Asn Glu Ile Ala Pro Leu Glu Pro Asp		
275	280	285
Ala Pro Pro Asp Ala Cys Glu Ala Ser Phe Asp Ala Val Ser Thr Ile		
290	295	300
Arg Gly Glu Leu Phe Phe Lys Ala Gly Phe Val Trp Arg Leu Arg		
305	310	315
Gly Gly Gln Leu Gln Pro Gly Tyr Pro Ala Leu Ala Ser Arg His Trp		320
325	330	335
Gln Gly Leu Pro Ser Pro Val Asp Ala Ala Phe Glu Asp Ala Gln Gly		
340	345	350
His Ile Trp Phe Phe Gln Gly Ala Gln Tyr Trp Val Tyr Asp Gly Glu		
355	360	365
Lys Pro Val Leu Gly Pro Ala Pro Leu Thr Glu Leu Gly Leu Val Arg		
370	375	380
Phe Pro Val His Ala Ala Leu Val Trp Gly Pro Glu Lys Asn Lys Ile		
385	390	395
Tyr Phe Phe Arg Gly Arg Asp Tyr Trp Arg Phe His Pro Ser Thr Arg		400
405	410	415
Arg Val Asp Ser Pro Val Pro Arg Arg Ala Thr Asp Trp Arg Gly Val		
420	425	430
Pro Ser Glu Ile Asp Ala Ala Phe Gln Asp Ala Asp Gly Tyr Ala Tyr		
435	440	445
Phe Leu Arg Gly Arg Leu Tyr Trp Lys Phe Asp Pro Val Lys Val Lys		
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Ala Leu Glu Gly Phe Pro Arg Leu Val Gly Pro Asp Phe Phe Gly Cys		
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Ala Glu Pro Ala Asn Thr Phe Leu		480
485		

<210> 207

<211> 3074

<212> DNA

<213> Homo sapiens

<400> 207

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<210> 208

<211> 660

<212> PRT

<213> Homo sapiens

<400> 208

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 Trp Pro Glu Leu Pro Glu Lys Ile Asp Ala Val Tyr Glu Ala Pro Gln
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 Ala Ser Thr Leu Glu Arg Gly Tyr Pro Lys Pro Leu Thr Ser Leu Gly
 545 550 555 560
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 Asn Lys Lys Thr Tyr Ile Phe Ala Gly Asp Lys Phe Trp Arg Tyr Asn
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 Glu Val Lys Lys Lys Met Asp Pro Gly Phe Pro Lys Leu Ile Ala Asp
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 Ala Trp Asn Ala Ile Pro Asp Asn Leu Asp Ala Val Val Asp Leu Gln
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 Gly Gly Gly His Ser Tyr Phe Phe Lys Gly Ala Tyr Tyr Leu Lys Leu
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<210> 209

<211> 4160

<212> DNA

<213> Homo sapiens

<400> 209

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<210> 210

<211> 328

<212> PRT

<213> Homo sapiens

<400> 210

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Gly	Ile	Ile	Glu	Lys	Arg	Arg	Asp	Arg	Ile	Asn	Ser	Leu
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Glu	Leu	Arg	Arg	Leu	Val	Pro	Thr	Ala	Phe	Glu	Lys	Gln
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Lys	Leu	Glu	Lys	Ala	Glu	Val	Leu	Gln	Met	Thr	Val	Asp
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Ala	Val	Asp	Phe	Arg	Ser	Ile	Gly	Phe	Arg	Glu	Cys	Leu
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Ile Arg Tyr Leu Gly Val Leu Glu Gly Pro Ser Ser Arg Ala Asp Pro
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 Val Arg Ile Arg Leu Leu Ser His Leu Asn Ser Tyr Ala Ala Glu Met
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 Glu Pro Ser Pro Thr Pro Thr Gly Pro Leu Ala Phe Pro Ala Trp Pro
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 Trp Ser Phe Phe His Ser Cys Pro Gly Leu Pro Ala Leu Ser Asn Gln
 180 185 190
 Leu Ala Ile Leu Gly Arg Val Pro Ser Pro Val Leu Pro Gly Val Ser
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 Ser Pro Ala Tyr Pro Ile Pro Ala Leu Arg Thr Ala Pro Leu Arg Arg
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 Ala Thr Gly Ile Ile Leu Pro Ala Arg Arg Asn Val Leu Pro Ser Arg
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 Gly Ala Ser Ser Thr Arg Arg Ala Arg Pro Leu Glu Arg Pro Ala Thr
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 Pro Val Pro Val Ala Pro Ser Ser Arg Ala Ala Arg Ser Ser His Ile
 260 265 270
 Ala Pro Leu Leu Gln Ser Ser Ser Pro Thr Pro Pro Gly Pro Thr Gly
 275 280 285
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<210> 211
<211> 5680
<212> DNA
<213> Homo sapiens

<400> 211

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<212> PRT
<213> Homo sapiens

<400> 212

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Thr Leu Leu Leu Ser Asn Asn Lys Ile Thr Gly Leu Arg Asn Gly Ser			
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Phe Leu Gly Leu Ser Leu Leu Glu Lys Leu Asp Leu Arg Asn Asn Ile			
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Ile Ser Thr Val Gln Pro Gly Ala Phe Leu Gly Leu Glu Leu Lys			
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Arg Leu Asp Leu Ser Asn Asn Arg Ile Gly Cys Leu Thr Ser Glu Thr			
130	135	140	
Phe Gln Gly Leu Pro Arg Leu Leu Arg Leu Asn Ile Ser Gly Asn Ile			
145	150	155	160
Phe Ser Ser Leu Gln Pro Gly Val Phe Asp Glu Leu Pro Ala Leu Lys			
165	170	175	
Val Val Asp Leu Gly Thr Glu Phe Leu Thr Cys Asp Cys His Leu Arg			
180	185	190	
Trp Leu Leu Pro Trp Ala Gln Asn Arg Ser Leu Gln Leu Ser Glu His			
195	200	205	
Thr Leu Cys Ala Tyr Pro Ser Ala Leu His Ala Gln Ala Leu Gly Ser			
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Leu Gln Glu Ala Gln Leu Cys Cys Glu Gly Ala Leu Glu Leu His Thr			
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His His Leu Ile Pro Ser Leu Arg Gln Val Val Phe Gln Gly Asp Arg			
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Leu Pro Phe Gln Cys Ser Ala Ser Tyr Leu Gly Asn Asp Thr Arg Ile			
260	265	270	
Arg Trp Tyr His Asn Arg Ala Pro Val Glu Gly Asp Glu Gln Ala Gly			
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Ile Leu Leu Ala Glu Ser Leu Ile His Asp Cys Thr Phe Ile Thr Ser			
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Glu Leu Thr Leu Ser His Ile Gly Val Trp Ala Ser Gly Glu Trp Glu			
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Cys Thr Val Ser Met Ala Gln Gly Asn Ala Ser Lys Lys Val Glu Ile			
325	330	335	
Val Val Leu Glu Thr Ser Ala Ser Tyr Cys Pro Ala Glu Arg Val Ala			
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Asn Asn Arg Gly Asp Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr			
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Ala Tyr Gln Ser Cys Leu Gln Tyr Pro Phe Thr Ser Val Pro Leu Gly
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 Arg Trp Glu Pro Gly Asp Tyr Ser His Cys Leu Tyr Thr Asn Asp Ile
 405 410 415
 Thr Arg Val Leu Tyr Thr Phe Val Leu Met Pro Ile Asn Ala Ser Asn
 420 425 430
 Ala Leu Thr Leu Ala His Gln Leu Arg Val Tyr Thr Ala Glu Ala Ala
 435 440 445
 Ser Phe Ser Asp Met Met Asp Val Val Tyr Val Ala Gln Met Ile Gln
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 Lys Phe Leu Gly Tyr Val Asp Gln Ile Lys Glu Leu Val Glu Val Met
 465 470 475 480
 Val Asp Met Ala Ser Asn Leu Met Leu Val Asp Glu His Leu Leu Trp
 485 490 495
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 500 505 510
 Glu Arg Ile Gly Gly Ala Ala Leu Ser Pro His Ala Gln His Ile Ser
 515 520 525
 Val Asn Ala Arg Asn Val Ala Leu Glu Ala Tyr Leu Ile Lys Pro His
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 Ser Tyr Val Gly Leu Thr Cys Thr Ala Phe Gln Arg Arg Glu Gly Gly
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 Pro Glu Pro Pro Ala Asp Gln Gln Leu Arg Phe Arg Cys Thr Thr Gly
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 Arg Pro Asn Val Ser Leu Ser Ser Phe His Ile Lys Asn Ser Val Ala
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 Ala Leu Ala Pro Pro Val Pro Pro Asp Cys Thr Leu Gln Leu Leu Val
 625 630 635 640
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 645 650 655
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 660 665 670
 Phe Ala Gly Thr Ser Gly Cys Gly Val Gly Asn Leu Thr Glu Pro Val
 675 680 685
 Ala Val Ser Leu Arg His Trp Ala Glu Gly Ala Glu Pro Val Ala Ala
 690 695 700
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 705 710 715 720
 Gly Cys Gln Leu Arg Ser Ser Gln Pro Asn Val Ser Ala Leu His Cys
 725 730 735
 Gln His Leu Gly Asn Val Ala Val Leu Met Glu Leu Ser Ala Phe Pro
 740 745 750
 Arg Glu Val Gly Gly Ala Gly Ala Gly Leu His Pro Val Val Tyr Pro
 755 760 765
 Cys Thr Ala Leu Leu Leu Cys Leu Phe Ala Thr Ile Ile Thr Tyr
 770 775 780
 Ile Leu Asn His Ser Ser Ile Arg Val Ser Arg Lys Gly Trp His Met
 785 790 795 800
 Leu Leu Asn Leu Cys Phe His Ile Ala Met Thr Ser Ala Val Phe Ala
 805 810 815
 Gly Gly Ile Thr Leu Thr Asn Tyr Gln Met Val Cys Gln Ala Val Gly
 820 825 830
 Ile Thr Leu His Tyr Ser Ser Leu Ser Thr Leu Leu Trp Met Gly Val
 835 840 845
 Lys Ala Arg Val Leu His Lys Glu Leu Thr Trp Arg Ala Pro Pro Pro

850	855	860
Gln Glu Gly Asp Pro Ala Leu Pro Thr Pro Ser Pro Met Leu Arg Phe		
865	870	875
Tyr Leu Ile Ala Gly Gly Ile Pro Leu Ile Ile Cys Gly Ile Thr Ala		880
885	890	895
Ala Val Asn Ile His Asn Tyr Arg Asp His Ser Pro Tyr Cys Trp Leu		
900	905	910
Val Trp Arg Pro Ser Leu Gly Ala Phe, Tyr Ile Pro Val Ala Leu Ile		
915	920	925
Leu Leu Ile Thr Trp Ile Tyr Phe Leu Cys Ala Gly Leu Arg Leu Arg		
930	935	940
Gly Pro Leu Ala Gln Asn Pro Lys Ala Gly Asn Ser Arg Ala Ser Leu		
945	950	955
Glu Ala Gly Glu Glu Leu Arg Gly Ser Thr Arg Leu Arg Gly Ser Gly		960
965	970	975
Pro Leu Leu Ser Asp Ser Gly Ser Leu Leu Ala Thr Gly Ser Ala Arg		
980	985	990
Val Gly Thr Pro Gly Pro Pro Glu Asp Gly Asp Ser Leu Tyr Ser Pro		
995	1000	1005
Gly Val Gln Leu Gly Ala Leu Val Thr Thr His Phe Leu Tyr Leu Ala		
1010	1015	1020
Met Trp Ala Cys Gly Ala Leu Ala Val Ser Gln Arg Trp Leu Pro Arg		
1025	1030	1035
Val Val Cys Ser Cys Leu Tyr Gly Val Ala Ala Ser Ala Leu Gly Leu		
1045	1050	1055
Phe Val Phe Thr His His Cys Ala Arg Arg Arg Asp Val Arg Ala Ser		
1060	1065	1070
Trp Arg Ala Cys Cys Pro Pro Ala Ser Pro Ala Ala Pro His Ala Pro		
1075	1080	1085
Pro Arg Ala Leu Pro Ala Ala Glu Asp Gly Ser Pro Val Phe Gly		
1090	1095	1100
Glu Gly Pro Pro Ser Leu Lys Ser Ser Pro Ser Gly Ser Ser Gly His		
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Pro Leu Ala Leu Gly Pro Cys Lys Leu Thr Asn Leu Gln Leu Ala Gln		
1125	1130	1135
Ser Gln Val Cys Glu Ala Gly Ala Ala Gly Gly Glu Gly Glu Pro		
1140	1145	1150
Glu Pro Ala Gly Thr Arg Gly Asn Leu Ala His Arg His Pro Asn Asn		
1155	1160	1165
Val His His Gly Arg Arg Ala His Lys Ser Arg Ala Lys Gly His Arg		
1170	1175	1180
Ala Gly Glu Ala Cys Gly Lys Asn Arg Leu Lys Ala Leu Arg Gly Gly		
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Asn Ser Pro Thr Asp Ser Tyr Leu Gly Ser Ser Arg Asn Ser Pro Gly		
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Ala Gly Leu Gln Leu Glu Gly Glu Pro Met Leu Thr Pro Ser Glu Gly		
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Ser Asp Thr Ser Ala Ala Pro Leu Ser Glu Ala Gly Arg Ala Gly Gln		
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Arg Arg Ser Ala Ser Arg Asp Ser Leu Lys Gly Gly Ala Leu Glu		
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Lys Glu Ser His Arg Arg Ser Tyr Pro Leu Asn Ala Ala Ser Leu Asn		
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Gly Ala Pro Lys Gly Gly Lys Tyr Asp Asp Val Thr Leu Met Gly Ala		
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<220>
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<400> 213

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 Tyr Asp Gly Lys Gly Val Gly Leu Gly Pro Gly Pro Met Gly Leu Met
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 Pro Gln Gly Ala Arg Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly Phe
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 Lys Gly Ile Arg Gly His Asn Gly Leu Asp Gly Leu Lys Gly Gln Pro
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 Phe Pro Gly Ala Pro Gly Pro Lys Gly Glu Ile Gly Ala Val Gly Asn
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 Ala Gly Pro Ala Gly Pro Ala Gly Pro Arg Gly Glu Val Gly Leu Pro
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 Gly Leu Ser Gly Pro Val Gly Pro Pro Gly Asn Pro Gly Ala Asn Gly
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 Leu Thr Gly Ala Lys Gly Ala Ala Gly Leu Pro Gly Val Ala Gly Ala
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 Pro Gly Leu Pro Gly Pro Arg Gly Ile Pro Gly Pro Val Gly Ala Ala
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 Gln Gly Pro Pro Gly Pro Ser Gly Glu Gly Lys Arg Gly Pro Asn
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 Ala Gly Leu Ala Gly Ala Arg Gly Ala Pro Gly Pro Asp Gly Asn Asn
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 Gly Ala Gln Gly Pro Pro Gly Pro Gln Gly Val Gln Gly Gly Lys Gly
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 Glu Gln Gly Pro Ala Gly Pro Pro Gly Phe Gln Gly Leu Pro Gly Pro
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 Ser Gly Pro Ala Gly Glu Val Gly Lys Pro Gly Glu Arg Gly Leu His
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 Gly Glu Phe Gly Leu Pro Gly Pro Ala Gly Pro Arg Gly Glu Arg Gly
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 Pro Pro Gly Glu Ser Gly Ala Ala Gly Pro Thr Gly Pro Ile Gly Ser
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 Arg Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly Asn Lys Gly Glu Pro

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Lys Gly Glu Pro Gly Leu Arg Gly Glu Ile Gly Asn Pro Gly Arg Asp		
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675	680	685
Ala Thr Gly Asp Arg Gly Glu Ala Gly Ala Ala Gly Pro Ala Gly Pro		
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Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Val Gly Pro Ala		
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Gly Pro Asn Gly Phe Ala Gly Pro Ala Gly Ala Ala Gly Gln Pro Gly		720
725	730	735
Ala Lys Gly Glu Arg Gly Ala Lys Gly Pro Lys Gly Glu Asn Gly Val		
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Val Gly Pro Thr Gly Pro Val Gly Ala Ala Gly Pro Ala Gly Pro Asn		
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Gly Pro Pro Gly Pro Ala Gly Ser Arg Gly Asp Gly Gly Pro Pro Gly		
770	775	780
Met Thr Gly Phe Pro Gly Ala Ala Gly Arg Thr Gly Pro Pro Gly Pro		
785	790	795
Ser Gly Ile Ser Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Lys Glu		800
805	810	815
Gly Leu Arg Gly Pro Arg Gly Asp Gln Gly Pro Val Gly Arg Thr Gly		
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Glu Val Gly Ala Val Gly Pro Pro Gly Phe Ala Gly Glu Lys Gly Pro		
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Ser Gly Glu Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly Pro Gln		
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Glu Arg Gly Leu Pro Gly Val Ala Gly Ala Val Gly Glu Pro Gly Pro		
885	890	895
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Gly Ser Pro Gly Val Asn Gly Ala Pro Gly Glu Ala Gly Arg Asp Gly		
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Asn Pro Gly Asn Asp Gly Pro Pro Gly Arg Asp Gly Gln Pro Gly His		
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Lys Gly Glu Arg Gly Tyr Pro Gly Asn Ile Gly Pro Val Gly Ala Ala		
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Gly Ala Pro Gly Pro His Gly Pro Val Gly Pro Ala Gly Lys His Gly		960
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Val Gly Pro Arg Gly Pro Ser Gly Pro Gln Gly Ile Arg Gly Asp Lys		
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Gly Glu Pro Gly Glu Lys Gly Pro Arg Gly Leu Pro Gly Leu Lys Gly		
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His Asn Gly Leu Gln Gly Leu Pro Gly Ile Ala Gly His His Gly Asp		
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Ala Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Val Ser		
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<400> 215

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<210> 216

<211> 1247

<212> PRT

<213> Homo sapiens

<400> 216

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Leu	Leu	Pro	Leu	Leu	Leu	Ala	Gly	Pro	Val	Gly	Cys	Leu	Ser	Arg	Gln	
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Glu	Leu	Phe	Pro	Phe	Gly	Pro	Gly	Gln	Gly	Asp	Leu	Glu	Leu	Glu	Asp	
							35			40				45		
Gly	Asp	Asp	Phe	Val	Ser	Pro	Ala	Leu	Glu	Leu	Ser	Gly	Ala	Leu	Arg	
							50			55				60		
Phe	Tyr	Asp	Arg	Ser	Asp	Ile	Asp	Ala	Val	Tyr	Val	Thr	Thr	Asn	Gly	
							65			70				80		
Ile	Ile	Ala	Thr	Ser	Glu	Pro	Pro	Ala	Lys	Glu	Ser	His	Pro	Gly	Leu	
							85			90				95		
Phe	Pro	Pro	Thr	Phe	Gly	Ala	Val	Ala	Pro	Phe	Leu	Ala	Asp	Leu	Asp	
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Thr	Thr	Asp	Gly	Leu	Gly	Lys	Val	Tyr	Tyr	Arg	Glu	Asp	Leu	Ser	Pro	
							115			120				125		
Ser	Ile	Thr	Gln	Arg	Ala	Ala	Glu	Cys	Val	His	Arg	Gly	Phe	Pro	Glu	
							130			135				140		
Ile	Ser	Phe	Gln	Pro	Ser	Ser	Ala	Val	Val	Val	Thr	Trp	Glu	Ser	Val	
							145			150				155		160
Ala	Pro	Tyr	Gln	Gly	Pro	Ser	Arg	Asp	Pro	Asp	Gln	Lys	Gly	Lys	Arg	
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Asn	Thr	Phe	Gln	Ala	Val	Leu	Ala	Ser	Ser	Asp	Ser	Ser	Ser	Tyr	Ala	
							180			185				190		
Ile	Phe	Leu	Tyr	Pro	Glu	Asp	Gly	Leu	Gln	Phe	His	Thr	Thr	Phe	Ser	
							195			200				205		
Lys	Lys	Glu	Asn	Asn	Gln	Val	Pro	Ala	Val	Val	Ala	Phe	Ser	Gln	Gly	
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Ser	Val	Gly	Phe	Leu	Trp	Lys	Ser	Asn	Gly	Ala	Tyr	Asn	Ile	Phe	Ala	
							225			230				235		240
Asn	Asp	Arg	Glu	Ser	Ile	Glu	Asn	Leu	Ala	Lys	Ser	Ser	Asn	Ser	Gly	
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Gln	Gln	Gly	Val	Trp	Val	Phe	Glu	Ile	Gly	Ser	Pro	Ala	Thr	Thr	Asn	
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Gly	Val	Val	Pro	Ala	Asp	Val	Ile	Leu	Gly	Thr	Glu	Asp	Gly	Ala	Glu	
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Tyr	Asp	Asp	Glu	Asp	Glu	Asp	Tyr	Asp	Leu	Ala	Thr	Thr	Arg	Leu	Gly	
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Leu	Glu	Asp	Val	Gly	Thr	Thr	Pro	Phe	Ser	Tyr	Lys	Ala	Leu	Arg	Arg	
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Gly	Gly	Ala	Asp	Thr	Tyr	Ser	Val	Pro	Ser	Val	Leu	Ser	Pro	Arg	Arg	
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Ala	Ala	Thr	Glu	Arg	Pro	Leu	Gly	Pro	Pro	Thr	Glu	Arg	Thr	Arg	Ser	
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Phe	Gln	Leu	Ala	Val	Glu	Thr	Phe	His	Gln	Gln	His	Pro	Gln	Val	Ile	
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Asp	Val	Asp	Glu	Val	Glu	Glu	Thr	Gly	Val	Val	Phe	Ser	Tyr	Asn	Thr	
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Asp	Ser	Arg	Gln	Thr	Cys	Ala	Asn	Asn	Arg	His	Gln	Cys	Ser	Val	His	
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Ala	Glu	Cys	Arg	Asp	Tyr	Ala	Thr	Gly	Phe	Cys	Cys	Ser	Cys	Val	Ala	
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Gly	Tyr	Thr	Gly	Asn	Gly	Arg	Gln	Cys	Val	Ala	Glu	Gly	Ser	Pro	Gln	

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Asn His Gly Arg Ser Tyr Thr Ala Ile Ser Thr Ile Pro Glu Thr Val			
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Gly Tyr Ser Leu Leu Pro Leu Ala Pro Val Gly Gly Ile Ile Gly Trp			
485	490	495	
Met Phe Ala Val Glu Gln Asp Gly Phe Lys Asn Gly Phe Ser Ile Thr			
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Phe Gly Ser Ser Val His Ile Glu Pro Tyr Thr Glu Leu Tyr His Tyr			
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Trp Arg Gln Thr Ile Thr Phe Gln Glu Cys Val His Asp Asp Ser Arg			
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Pro Arg Thr Gln Phe Thr Cys Glu Cys Ser Ile Gly Phe Arg Gly Asp			
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Gly Arg Thr Cys Tyr Asp Ile Asp Glu Cys Ser Glu Gln Pro Ser Val			
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Cys Gly Ser His Thr Ile Cys Asn Asn His Pro Gly Thr Phe Arg Cys			
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Glu Cys Val Glu Gly Tyr Gln Phe Ser Asp Glu Gly Thr Cys Val Ala			
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Val Val Asp Gin Arg Pro Ile Asn Tyr Cys Glu Thr Gly Leu His Asn			
755	760	765	
Cys Asp Ile Pro Gln Arg Ala Gln Cys Ile Tyr Thr Gly Gly Ser Ser			
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Tyr Thr Cys Ser Cys Leu Pro Gly Phe Ser Gly Asp Gly Gln Ala Cys			
785	790	795	800
Gln Asp Val Asp Glu Cys Gln Pro Ser Arg Cys His Pro Asp Ala Phe			
805	810	815	
Cys Tyr Asn Thr Pro Gly Ser Phe Thr Cys Gln Cys Lys Pro Gly Tyr			
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Gln Gly Asp Gly Phe Arg Cys Val Pro Gly Glu Val Glu Lys Thr Arg			
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Cys Gln His Glu Arg Glu His Ile Leu Gly Ala Ala Gly Ala Thr Asp			
850	855	860	
Pro Gln Arg Pro Ile Pro Pro Gly Leu Phe Val Pro Glu Cys Asp Ala			
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His Gly His Tyr Ala Pro Thr Gln Cys His Gly Ser Thr Gly Tyr Cys			
885	890	895	
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 Gln Gly Pro Ala Val Pro Thr Ala Val Ile Pro Leu Pro Pro Gly Thr
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 965 970 975
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 980 985 990
 Tyr Trp Thr Asp Ile Thr Glu Pro Ser Ile Gly Arg Ala Ser Leu His
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 Ser Val Arg Gly Asn Leu Tyr Trp Thr Asp Trp Asn Arg Asp Asn Pro
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<400> 217

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 35 40 45
 Thr Ile Gly Glu Glu His Phe Gln Leu Val Arg Glu Phe Leu Tyr Asp
 50 55 60
 Val Val Lys Ser Leu Ala Val Gly Glu Asn Asp Phe His Phe Ala Leu
 65 70 75 80

Val Gln Phe Asn Gly Asn Pro His Thr Glu Phe Leu Leu Asn Thr Tyr
 85 90 95
 Arg Thr Lys Gln Glu Val Leu Ser His Ile Ser Asn Met Ser Tyr Ile
 100 105 110
 Gly Gly Thr Asn Gln Thr Gly Lys Gly Leu Glu Tyr Ile Met Gln Ser
 115 120 125
 His Leu Thr Lys Ala Ala Gly Ser Arg Ala Gly Asp Gly Val Pro Gln
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 Val Ile Val Val Leu Thr Asp Gly His Ser Lys Asp Gly Leu Ala Leu
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 Pro Ser Ala Glu Leu Lys Ser Ala Asp Val Asn Val Phe Ala Ile Gly
 165 170 175
 Val Glu Asp Ala Asp Glu Gly Ala Leu Lys Glu Ile Ala Ser Glu Pro
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 Leu Asn Met His Met Phe Asn Leu Glu Asn Phe Thr Ser Leu His Asp
 195 200 205
 Ile Val Gly Asn Leu Val Ser Cys Val His Ser Ser Val Ser Pro Glu
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 Arg Ala Gly Asp Thr Glu Thr Leu Lys Asp Ile Thr Ala Gln Asp Ser
 225 230 235 240
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 Glu Pro Arg Thr Met Phe Ser Leu Asp Thr Tyr Ser Thr Lys Ala Gln
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Asn Asp Asn Ile Arg Val Gly	Leu Val Gln Phe Ser Asp Thr Pro Val		
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Thr Glu Phe Ser Leu Asn Thr Tyr Gln Thr Lys	Ser Asp Ile Leu Gly		
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Ser Ala Leu Ser Tyr Val Tyr Ala Asn His	Phe Thr Glu Ala Gly Gly		
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Thr Thr Tyr Val Ser Gly Gly Val	Glu Glu Val Pro Leu Ala Gln Pro		
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Glu Ser Lys Arg Asp Ile Leu Phe Leu Phe Asp Gly	Ser Ala Asn Leu		
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Val Gly Gln Phe Pro Val Val Arg Asp Phe Leu	Tyr Lys Ile Ile Asp		
850	855	860	
Glu Leu Asn Val Lys Pro Glu Gly Thr Arg	Ile Ala Val Ala Gln Tyr		
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Ser Asp Asp Val Lys Val Glu Ser Arg Phe Asp Glu	His Gln Ser Lys		
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Pro Glu Ile Leu Asn Leu Val Lys Arg Met Lys	Ile Lys Thr Gly Lys		
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Val Lys Ser Ala Gly Ser Arg Ile Glu Asp Gly	Val Leu Gln Phe Leu		
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Met Tyr Asp Arg Pro Leu Arg Leu Asn Leu Leu Asp Leu Asp Tyr Glu			
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Leu Ala Glu Gln Leu Asp Asn Ile Ala Glu Lys Ala Cys Cys Gly Val			
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 Lys Gly Asn Lys Gly Gly Pro Gly Gln Pro Gly Phe Glu Gly Glu Gln
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 Arg Gly Ala Pro Gly Glu Arg Gly Arg Thr Gly Pro Leu Gly Arg Lys
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 Gly Glu Pro Gly Glu Pro Gly Pro Lys Gly Gly Ile Gly Asn Pro Gly
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 Pro Arg Gly Glu Thr Gly Asp Asp Gly Arg Asp Gly Val Gly Ser Glu
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 Gly Arg Arg Gly Lys Lys Gly Glu Arg Gly Phe Pro Gly Tyr Pro Gly
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 Thr Glu Leu Ala Phe Ala Leu Asp Thr Ser Glu Gly Val Asn Gln Asp
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 2485 2490 2495
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 2500 2505 2510
 Val Phe Phe Ser Asn Thr Pro Thr Arg Ala Ser Pro Gln Leu Arg Glu

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Arg Gln Glu Asp Arg Gln Leu Ile Asn Ala Leu Gln Ile Asn Asn Thr		
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Ala Val Gly His Ala Leu Val Leu Pro Ala Gly Arg Asp Leu Thr Asp		
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Phe Leu Glu Asn Val Leu Thr Cys His Val Cys Leu Asp Ile Cys Asn		
2580	2585	2590
Ile Asp Pro Ser Cys Gly Phe Gly Ser Trp Arg Pro Ser Phe Arg Asp		
2595	2600	2605
Arg Arg Ala Ala Gly Ser Asp Val Asp Ile Asp Met Ala Phe Ile Leu		
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Asp Ser Ala Glu Thr Thr Leu Phe Gln Phe Asn Glu Met Lys Lys		
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Tyr Ile Ala Tyr Leu Val Arg Gln Leu Asp Met Ser Pro Asp Pro Lys		
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Ala Ser Gln His Phe Ala Arg Val Ala Val Val Gln His Ala Pro Ser		
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Glu Ser Val Ser Met Pro Pro Val Lys Val Glu Phe Ser Leu Thr Asp		
2675	2680	2685
Tyr Gly Ser Lys Glu Lys Leu Val Asp Phe Leu Ser Arg Gly Met Thr		
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Gln Leu Gln Gly Thr Arg Ala Leu Gly Ser Ala Ile Glu Tyr Thr Ile		
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Leu Gly Ile Gly Arg Lys Val Asn Ile Lys Glu Val Tyr Thr Phe Ala		
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Ser Glu Pro Asn Asp Val Phe Phe Lys Leu Val Asp Lys Ser Thr Glu		
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 Tyr Leu Arg Ser Gln Val Arg Ala Thr Tyr His Gly Ser Phe Ser Thr
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 Lys Lys Ser Gln Pro Pro Pro Gln Pro Ala Arg Ser Ala Ser Ser
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 <211> 2806
 <212> DNA
 <213> Homo sapiens

<400> 219

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 <213> Homo sapiens

<400> 220
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 Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Pro Ile
 35 40 45
 Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe
 50 55 60
 Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe
 65 70 75 80
 Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser
 85 90 95
 Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly His Ser
 100 105 110
 Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val
 115 120 125
 Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser Trp Leu Leu
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 Leu

<210> 221
 <211> 736
 <212> DNA
 <213> Homo sapiens

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<212> DNA
<213> *Homo sapiens*

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<210> 223
<211> 141
<212> PRT
<213> *Homo sapiens*

<400> 223
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 35 40 45
 he Ala Ile Ser Glu Tyr Asn Lys Ala Thr Glu Asp Glu Tyr Tyr
 0 55 60
 rg Pro Leu Gln Val Leu Arg Ala Arg Glu Gln Thr Phe Gly Gly
 70 75 80
 sn Tyr Phe Phe Asp Val Glu Val Gly Arg Thr Ile Cys Thr Lys
 85 90 95
 ln Pro Asn Leu Asp Thr Cys Ala Phe His Glu Gln Pro Glu Leu
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 ys Lys Gln Leu Cys Ser Phe Glu Ile Tyr Glu Val Pro Trp Glu
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<210> 224
<211> 141
<212> PRT
<213> *Homo sapiens*

<400> 224
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 20 25 30
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 35 40 45
 His Phe Ala Ile Ser Glu Tyr Asn Lys Ala Thr Lys Asp Asp Tyr Tyr
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 Arg Arg Pro Leu Arg Val Leu Arg Ala Arg Gln Gln Thr Val Gly Gly

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Val Asn Tyr Phe Phe Asp Val Glu Val Gly Arg Thr Ile Cys Thr Lys			
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Ser Gln Pro Asn Leu Asp Thr Cys Ala Phe His Glu Gln Pro Glu Leu			
100	105	110	
Gln Lys Lys Gln Leu Cys Ser Phe Glu Ile Tyr Glu Val Pro Trp Glu			
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<210> 225

<211> 5460

<212> DNA

<213> Homo sapiens

<400> 225

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Phe Gly Glu Cys Cys Ala Val Cys Pro Gln Pro Pro Thr Ala Pro Thr		
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 <212> DNA

<213> Homo sapiens

<400> 227

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attttacac aaggtaaaacg tggtaaggc catcggggaa tt当地 gctccaa gcaagatagct	6060
ccctctgagg aaccaaaggaa agcaagttt caccatttctt gaaagactgg tataggaat	6120
ttt当地 ttcttctt cttt当地 gtgttcatc acatgtgc当地 taacacagaac aagctgtgtg tcatc当地	6180
ttgtactgtg ggctc当地 gaaa ccgtgagaga gccccccaccc tggacaccgg ctctaggggc	6240
acaggaaaag gaacgttcc aggcattttgc tctccaggc tccc当地 ctgc当地 caggcacgt	6300
ctgccc当地 ctgggg gaggtaaatgc ggagatgtca cgaactgtgc ccaacgc当地 ttatagccag	6360
ggctctacta actactcact aaaaacacgt attgttgc当地 ttctccaggc ttaagctata	6420
gccatgttaa aagtactgt gcatttatttcc tcaagcatcaa ataccttgc当地 acgttctc	6480
tgc当地 ctgttta gtgc当地 atttttctt gatactgtaa agaatatatc cagtagttaa	6540
atgaatgttca tataaaatctt ttgtatagtc attttctcg ctc当地 tttaat atcatctca	6600
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aaa	6663

<210> 228
 <211> 1202
 <212> PRT
 <213> Homo sapiens

<400> 228

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			20				25						30		
Val	Phe	Gly	Lys	Glu	Asp	Leu	Ser	Lys	Asp	Asp	Arg	Phe	Pro	Asp	Tyr
		35				40					45				
Gly	Lys	Val	Glu	Leu	Val	Phe	Ser	Ala	Thr	Pro	Glu	Lys	Ile	Gln	Gly
	50				55						60				
Ser	Glu	His	Leu	Tyr	Asn	Asp	His	Gly	Val	Ile	Val	Asp	Tyr	Asn	Thr
65				70				75					80		
Thr	Asp	Pro	Leu	Ile	Arg	Trp	Asp	Ser	Tyr	Glu	Asn	Leu	Ser	Ala	Asp
				85				90					95		
Gly	Glu	Val	Leu	His	Thr	Gln	Gly	Pro	Val	Asp	Gly	Ser	Leu	Tyr	Ala
	100				105				105				110		
Lys	Val	Arg	Lys	Lys	Ser	Ser	Ser	Asp	Pro	Gly	Ile	Pro	Gly	Gly	Pro
	115					120						125			
Gln	Ala	Ile	Pro	Ala	Thr	Asn	Ser	Pro	Asp	His	Ser	Asp	His	Thr	Leu
	130				135							140			
Ser	Val	Ser	Ser	Asp	Ser	Gly	His	Ser	Thr	Ala	Ser	Ala	Arg	Thr	Asp
145					150				155				160		
Lys	Thr	Glu	Glu	Arg	Leu	Ala	Pro	Gly	Thr	Arg	Arg	Gly	Leu	Ser	Ala
				165				170					175		
Gln	Glu	Lys	Ala	Glu	Leu	Asp	Gln	Leu	Ser	Gly	Phe	Gly	Leu	Glu	
	180				185						190				
Asp	Pro	Gly	Ser	Ser	Leu	Lys	Glu	Met	Thr	Asp	Ala	Arg	Ser	Lys	Tyr
	195					200				205					
Ser	Gly	Thr	Arg	His	Val	Val	Pro	Ala	Gln	Val	His	Val	Asn	Gly	Asp
	210				215						220				
Ala	Ala	Leu	Lys	Asp	Arg	Glu	Thr	Asp	Ile	Leu	Asp	Asp	Glu	Met	Pro
	225				230				235				240		
His	His	Asp	Leu	His	Ser	Val	Asp	Ser	Leu	Gly	Thr	Leu	Ser	Ser	Ser
					245				250				255		
Glu	Gly	Pro	Gln	Ser	Ala	His	Leu	Gly	Pro	Phe	Thr	Cys	His	Lys	Ser
	260					265					270				
Ser	Gln	Asn	Ser	Leu	Leu	Ser	Asp	Gly	Phe	Gly	Ser	Asn	Val	Gly	Glu
	275					280					285				
Asp	Pro	Gln	Gly	Thr	Leu	Val	Pro	Asp	Leu	Gly	Leu	Gly	Met	Asp	Gly
	290				295					300					
Pro	Tyr	Glu	Arg	Glu	Arg	Thr	Phe	Gly	Ser	Arg	Glu	Pro	Lys	Gln	Pro
	305				310				315				320		
Gln	Pro	Leu	Leu	Arg	Lys	Pro	Ser	Val	Ser	Ala	Gln	Met	Gln	Ala	Tyr
					325				330				335		
Gly	Gln	Ser	Ser	Tyr	Ser	Thr	Gln	Thr	Trp	Val	Arg	Gln	Gln	Gln	Met
					340			345				350			
Val	Val	Ala	His	Gln	Tyr	Ser	Phe	Ala	Pro	Asp	Gly	Glu	Ala	Arg	Leu
					355			360				365			
Val	Ser	Arg	Cys	Pro	Ala	Asp	Asn	Pro	Gly	Leu	Val	Gln	Ala	Gln	Pro
					370			375			380				
Arg	Val	Pro	Leu	Thr	Pro	Thr	Arg	Gly	Thr	Ser	Arg	Val	Ala	Val	
	385				390					395			400		
Gln	Arg	Gly	Val	Gly	Ser	Gly	Pro	His	Pro	Pro	Asp	Thr	Gln	Gln	Pro
					405				410			415			
Ser	Pro	Ser	Lys	Ala	Phe	Lys	Pro	Arg	Phe	Pro	Gly	Asp	Gln	Val	Val
					420			425				430			
Asn	Gly	Ala	Gly	Pro	Glu	Leu	Ser	Thr	Gly	Pro	Ser	Pro	Gly	Ser	Pro
					435			440				445			
Thr	Leu	Asp	Ile	Asp	Gln	Ser	Ile	Glu	Gln	Leu	Asn	Arg	Leu	Ile	Leu
	450				455						460				
Glu	Leu	Asp	Pro	Thr	Phe	Glu	Pro	Ile	Pro	Thr	His	Met	Asn	Ala	Leu

465	470	475	480
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Leu Arg Ala Ser Ser Arg Leu Pro Asp Thr Gly Glu Gly Pro Ser Arg			
500	505	510	
Ala Thr Gly Arg Gln Gly Ser Ser Ala Glu Gln Pro Leu Gly Gly Arg			
515	520	525	
Leu Arg Lys Leu Ser Leu Gly Gln Tyr Asp Asn Asp Ala Gly Gly Gln			
530	535	540	
Leu Pro Phe Ser Lys Cys Ala Trp Gly Lys Ala Gly Val Asp Tyr Ala			
545	550	555	560
Pro Asn Leu Pro Pro Phe Pro Ser Pro Ala Asp Val Lys Glu Thr Met			
565	570	575	
Thr Pro Gly Tyr Pro Gln Asp Leu Asp Ile Ile Asp Gly Arg Ile Leu			
580	585	590	
Ser Ser Lys Glu Ser Met Cys Ser Thr Pro Ala Phe Pro Val Ser Pro			
595	600	605	
Glu Thr Pro Tyr Val Lys Thr Ala Leu Arg His Pro Pro Phe Ser Pro			
610	615	620	
Pro Glu Pro Pro Leu Ser Ser Pro Ala Ser Gln His Lys Gly Gly Arg			
625	630	635	640
Glu Pro Arg Ser Cys Pro Glu Thr Leu Thr His Ala Val Gly Met Ser			
645	650	655	
Glu Ser Pro Ile Gly Pro Lys Ser Thr Met Leu Arg Ala Asp Ala Ser			
660	665	670	
Ser Thr Pro Ser Phe Gln Gln Ala Phe Ala Ser Ser Cys Thr Ile Ser			
675	680	685	
Ser Asn Gly Pro Gly Gln Arg Arg Glu Ser Ser Ser Ala Glu Arg			
690	695	700	
Gln Trp Val Glu Ser Ser Pro Lys Pro Met Val Ser Leu Leu Gly Ser			
705	710	715	720
Gly Arg Pro Thr Gly Ser Pro Leu Ser Ala Glu Phe Ser Gly Thr Arg			
725	730	735	
Lys Asp Ser Pro Val Leu Ser Cys Phe Pro Pro Ser Glu Leu Gln Ala			
740	745	750	
Pro Phe His Ser His Glu Leu Ser Leu Ala Glu Pro Pro Asp Ser Leu			
755	760	765	
Ala Pro Pro Ser Ser Gln Ala Phe Leu Gly Phe Gly Thr Ala Pro Val			
770	775	780	
Gly Ser Gly Leu Pro Pro Glu Glu Asp Leu Gly Ala Leu Leu Ala Asn			
785	790	795	800
Ser His Gly Ala Ser Pro Thr Pro Ser Ile Pro Leu Thr Ala Thr Gly			
805	810	815	
Ala Ala Asp Asn Gly Phe Leu Ser His Asn Phe Leu Thr Val Ala Pro			
820	825	830	
Gly His Ser Ser His His Ser Pro Gly Leu Gln Gly Gln Gly Val Thr			
835	840	845	
Leu Pro Gly Gln Pro Pro Leu Pro Glu Lys Lys Arg Ala Ser Glu Gly			
850	855	860	
Asp Arg Ser Leu Gly Ser Val Ser Pro Ser Ser Ser Gly Phe Ser Ser			
865	870	875	880
Pro His Ser Gly Ser Thr Ile Ser Ile Pro Phe Pro Asn Val Leu Pro			
885	890	895	
Asp Phe Ser Lys Ala Ser Glu Ala Ala Ser Pro Leu Pro Asp Ser Pro			
900	905	910	
Gly Asp Lys Leu Val Ile Val Lys Phe Val Gln Asp Thr Ser Lys Phe			
915	920	925	
Trp Tyr Lys Ala Asp Ile Ser Arg Glu Gln Ala Ile Ala Met Leu Lys			
930	935	940	
Asp Lys Glu Pro Gly Ser Phe Ile Val Arg Asp Ser His Ser Phe Arg			
945	950	955	960

Gly Ala Tyr Gly Leu Ala Met Lys Val Ala Thr Pro Pro Pro Ser Val
 965 970 975
 Leu Gln Leu Asn Lys Lys Ala Gly Asp Leu Ala Asn Glu Leu Val Arg
 980 985 990
 His Phe Leu Ile Glu Cys Thr Pro Lys Gly Val Arg Leu Lys Gly Cys
 995 1000 1005
 Ser Asn Glu Pro Tyr Phe Gly Ser Leu Thr Ala Leu Val Cys Gln His
 1010 1015 1020
 Ser Ile Thr Pro Leu Ala Leu Pro Cys Lys Leu Leu Ile Pro Glu Arg
 1025 1030 1035 1040
 Asp Pro Leu Glu Glu Ile Ala Glu Ser Ser Pro Gln Thr Ala Ala Asn
 1045 1050 1055
 Ser Ala Ala Glu Leu Leu Lys Gln Gly Ala Ala Cys Asn Val Trp Tyr
 1060 1065 1070
 Leu Asn Ser Val Glu Met Glu Ser Leu Thr Gly His Gln Ala Ile Gln
 1075 1080 1085
 Lys Ala Leu Ser Ile Thr Leu Val Gln Glu Pro Pro Val Ser Thr
 1090 1095 1100
 Val Val His Phe Lys Val Ser Ala Gln Gly Ile Thr Leu Thr Asp Asn
 1105 1110 1115 1120
 Gln Arg Lys Leu Phe Phe Arg Arg His Tyr Pro Val Asn Ser Val Ile
 1125 1130 1135
 Phe Cys Ala Leu Asp Pro Gln Asp Arg Lys Trp Ile Lys Asp Gly Pro
 1140 1145 1150
 Ser Ser Lys Val Phe Gly Phe Val Ala Arg Lys Gln Gly Ser Ala Thr
 1155 1160 1165
 Asp Asn Val Cys His Leu Phe Ala Glu His Asp Pro Glu Gln Pro Ala
 1170 1175 1180
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 1185 1190 1195 1200
 Lys Val

<210> 229
 <211> 2320
 <212> DNA
 <213> Homo sapiens

<400> 229

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tggatgggct	gccaaaggga	ccgtgcgggg	ctggAACCGG	agagcccgag	agagccctgg	240
gcatgtgtca	gagccggaca	ggaccaggct	gagccaggac	ctgggtgggg	gcaccctggc	300
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gtcccgctc	tatggccca	gcgagccca	cagccggaa	ctgtgggttag	atgtggccga	420
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<210> 230

<211> 500

<212> PRT

<213> Homo sapiens

<400> 230

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					20			25				30			
Ser	Gly	Trp	Ala	Ala	Lys	Gly	Thr	Val	Arg	Gly	Trp	Asn	Arg	Arg	Ala
					35			40			45				
Arg	Glu	Ser	Pro	Gly	His	Val	Ser	Glu	Pro	Asp	Arg	Thr	Gln	Leu	Ser
					50			55			60				
Gln	Asp	Leu	Gly	Gly	Gly	Thr	Leu	Ala	Met	Asp	Thr	Leu	Pro	Asp	Asn
					65			70			75			80	
Arg	Thr	Arg	Val	Val	Glu	Asp	Asn	His	Ser	Tyr	Tyr	Val	Ser	Arg	Leu
					85			90			95				
Tyr	Gly	Pro	Ser	Glu	Pro	His	Ser	Arg	Glu	Leu	Trp	Val	Asp	Val	Ala
					100			105			110				
Glu	Ala	Asn	Arg	Ser	Gln	Val	Lys	Ile	His	Thr	Ile	Leu	Ser	Asn	Thr
					115			120			125				
His	Arg	Gln	Ala	Ser	Arg	Val	Val	Leu	Ser	Phe	Asp	Phe	Pro	Phe	Tyr
					130			135			140				
Gly	His	Pro	Leu	Arg	Gln	Ile	Thr	Ile	Ala	Thr	Gly	Gly	Phe	Ile	Phe
					145			150			155			160	
Met	Gly	Asp	Val	Ile	His	Arg	Met	Leu	Thr	Ala	Thr	Gln	Tyr	Val	Ala
					165			170			175				
Pro	Leu	Met	Ala	Asn	Phe	Asn	Pro	Gly	Tyr	Ser	Asp	Asn	Ser	Thr	Val
					180			185			190				
Val	Tyr	Phe	Asp	Asn	Gly	Thr	Val	Phe	Val	Val	Gln	Trp	Asp	His	Val
					195			200			205				
Tyr	Leu	Gln	Gly	Trp	Glu	Asp	Lys	Gly	Ser	Phe	Thr	Phe	Gln	Ala	Ala
					210			215			220				
Leu	His	His	Asp	Gly	Arg	Ile	Val	Phe	Ala	Tyr	Lys	Glu	Ile	Pro	Met
					225			230			235			240	
Ser	Val	Pro	Glu	Ile	Ser	Ser	Ser	Gln	His	Pro	Val	Lys	Thr	Gly	Leu
					245			250			255				
Ser	Asp	Ala	Phe	Met	Ile	Leu	Asn	Pro	Ser	Pro	Asp	Val	Pro	Glu	Ser
					260			265			270				
Arg	Arg	Arg	Ser	Ile	Phe	Glu	Tyr	His	Arg	Ile	Glu	Leu	Asp	Pro	Ser
					275			280			285				
Lys	Val	Thr	Ser	Met	Ser	Ala	Val	Glu	Phe	Thr	Pro	Leu	Pro	Thr	Cys

290	295	300	
Leu	Gln	His	Arg Ser Cys Asp Ala Cys Met Ser Ser Asp Leu Thr Phe
305			310 315 320
Asn	Cys	Ser	Trp Cys His Val Leu Gln Arg Cys Ser Ser Gly Phe Asp
			325 330 335
Arg	Tyr	Arg	Gln Glu Trp Met Asp Tyr Gly Cys Ala Gln Glu Ala Glu
			340 345 350
Gly	Arg	Met	Cys Glu Asp Phe Gln Asp Glu Asp His Asp Ser Ala Ser
			355 360 365
Pro	Asp	Thr	Phe Ser Pro Tyr Asp Gly Asp Leu Thr Thr Thr Ser
			370 375 380
Ser	Ser	Leu	Phe Ile Asp Ser Leu Thr Thr Glu Asp Asp Thr Lys Leu
385			390 395 400
Asn	Pro	Tyr	Ala Gly Gly Asp Gly Leu Gln Asn Asn Leu Ser Pro Lys
			405 410 415
Thr	Lys	Gly	Thr Pro Val His Leu Gly Thr Ile Val Gly Ile Val Leu
			420 425 430
Ala	Val	Leu	Leu Val Ala Ala Ile Ile Leu Ala Gly Ile Tyr Ile Asn
			435 440 445
Gly	His	Pro	Thr Ser Asn Ala Ala Leu Phe Phe Ile Glu Arg Arg Pro
			450 455 460
His	His	Trp	Pro Ala Met Lys Phe Arg Ser His Pro Asp His Ser Thr
465			470 475 480
Tyr	Ala	Glu	Val Glu Pro Ser Gly His Glu Lys Glu Gly Phe Met Glu
			485 490 495
Ala	Glu	Gln	Cys
			500

<210> 231
 <211> 5540
 <212> DNA
 <213> Homo sapiens

<400> 231

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tccagtggtct	ctctttggcc	actctggtgc	tcatctgcgc	ccggcaaggg	ggacgcagg	240
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gaagtgtgtct	gcaccactgg	aatgaaatct	attactttgt	ggaacagttt	gctcacaaat	360
tcatcagccc	acagttgaga	atgtccttta	ttgttttctc	cacccgagga	acaaccttaa	420
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tccatgaaga	tcttttttcc	tattcagaga	gggaggctaa	tagtctcga	gatcttggt	660
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acagggtcct	ctgcagcttc	aagatcaatg	actcggteac	actcaatgag	aagcccttt	960
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 <213> Homo sapiens

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 Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
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 Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Leu Gln Lys Val
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 Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
 115 120 125
 Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
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 Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
 145 150 155 160
 Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
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 Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
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 Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
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 Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
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 Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
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 Gly Leu Pro Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly

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		Glu		
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		Lys		
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		Ala		
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			Glu	
			Tyr	
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			Glu	
			Pro	
			Arg	
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			Arg	
			Arg	
			Pro	
			Ser	
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			Arg	
			Lys	
			Trp	
			Tyr	
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			Leu	
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			Ala	
			Leu	
			Trp	
			Val	
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			Val	
			Met	
			Arg	
			Pro	
			Gln	
			Pro	
			Gly	
			Asp	
			Thr	
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			Arg	
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			Asn	
			Gln	
			Pro	
			Ala	
			Lys	
			Tyr	
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			Tyr	
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			Thr	
			Ser	
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			Pro	
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			Ala	
			Pro	
	500	505	510	
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			Pro	
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			Cys	
			Pro	
			Ser	
			Ala	
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			Pro	
			Ser	
			Pro	
			Ser	
			Thr	
			Leu	
			Pro	
			Pro	
			Pro	
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			Asn	
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			Ala	
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5086

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<400> 234

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Gln	Gly	Pro	Pro	Gly	Pro	Ser	Gly	Glu	Glu	Gly	Lys	Arg	Gly	Pro	Asn
						370			375				380		
Gly	Glu	Ala	Gly	Ser	Ala	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Leu	Arg	Gly
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Ser	Pro	Gly	Ser	Arg	Gly	Leu	Pro	Gly	Ala	Asp	Gly	Arg	Ala	Gly	Val

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420	425	430	
Gly Pro Asn Gly Asp Ala Gly Arg Pro Gly Glu Pro Gly Leu Met Gly			
435	440	445	
Pro Arg Gly Leu Pro Gly Ser Pro Gly Asn Ile Gly Pro Ala Gly Lys			
450	455	460	
Glu Gly Pro Val Gly Leu Pro Gly Ile Asp Gly Arg Pro Gly Pro Ile			
465	470	475	480
Gly Pro Ala Gly Ala Arg Gly Glu Pro Gly Asn Ile Gly Phe Pro Gly			
485	490	495	
Pro Lys Gly Pro Thr Gly Asp Pro Gly Lys Asn Gly Asp Lys Gly His			
500	505	510	
Ala Gly Leu Ala Gly Ala Arg Gly Ala Pro Gly Pro Asp Gly Asn Asn			
515	520	525	
Gly Ala Gln Gly Pro Pro Gly Pro Gln Gly Val Gln Gly Gly Lys Gly			
530	535	540	
Glu Gln Gly Pro Ala Gly Pro Pro Gly Phe Gln Gly Leu Pro Gly Pro			
545	550	555	560
Ser Gly Pro Ala Gly Glu Val Gly Lys Pro Gly Glu Arg Gly Leu His			
565	570	575	
Gly Glu Phe Gly Leu Pro Gly Pro Ala Gly Pro Arg Gly Glu Arg Gly			
580	585	590	
Pro Pro Gly Glu Ser Gly Ala Ala Gly Pro Thr Gly Pro Ile Gly Ser			
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Arg Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly Asn Lys Gly Glu Pro			
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Gly Val Val Gly Ala Val Gly Thr Ala Gly Pro Ser Gly Pro Ser Gly			
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Leu Pro Gly Glu Arg Gly Ala Ala Gly Ile Pro Gly Gly Lys Gly Glu			
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Lys Gly Glu Pro Gly Leu Arg Gly Glu Ile Gly Asn Pro Gly Arg Asp			
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675	680	685	
Ala Thr Gly Asp Arg Gly Glu Ala Gly Ala Ala Gly Pro Ala Gly Pro			
690	695	700	
Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Val Gly Pro Ala			
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Gly Pro Asn Gly Phe Ala Gly Pro Ala Gly Ala Ala Gly Gln Pro Gly			
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Glu Val Gly Ala Val Gly Pro Pro Gly Phe Ala Gly Glu Lys Gly Pro			
835	840	845	
Ser Gly Glu Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly Pro Gln			
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Gly Leu Leu Gly Ala Pro Gly Ile Leu Gly Leu Pro Gly Ser Arg Gly			
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Glu Arg Gly Leu Pro Gly Val Ala Gly Ala Val Gly Glu Pro Gly Pro			
885	890	895	

Leu Gly Ile Ala Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Ala Val
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 Lys Gly Glu Arg Gly Tyr Pro Gly Asn Ile Gly Pro Val Gly Ala Ala
 945 950 955 960
 Gly Ala Pro Gly Pro His Gly Pro Val Gly Pro Ala Gly Lys His Gly
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 Gly Glu Pro Gly Glu Lys Gly Pro Arg Gly Leu Pro Gly Leu Lys Gly
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 His Asn Gly Leu Gln Gly Leu Pro Gly Ile Ala Gly His His Gly Asp
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 1125 1130 1135
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 35 40 45
 Pro Asp Lys Ala Arg Leu Leu Arg Gln Tyr Asp Asn Glu Lys Lys Trp
 50 55 60
 Asp Leu Ile Cys Asp Gln Glu Arg Phe Gln Val Lys Asn Pro Pro His
 65 70 75 80
 Thr Tyr Ile Gln Lys Leu Gln Ser Phe Leu Asp Pro Ser Val Thr Arg
 85 90 95
 Lys Lys Phe Arg Arg Arg Val Gln Glu Ser Thr Lys Val Leu Arg Glu
 100 105 110
 Leu Glu Ile Ser Leu Arg Thr Asn His Ile Gly Trp Val Arg Glu Phe
 115 120 125
 Leu Asn Asp Glu Asn Lys Gly Leu Asp Val Leu Val Asp Tyr Leu Ser
 130 135 140
 Phe Ala Gln Cys Ser Val Met Phe Asp Phe Glu Gly Leu Glu Ser Gly
 145 150 155 160
 Asp Asp Gly Ala Phe Asp Lys Leu Arg Ser Trp Ser Arg Ser Ile Glu
 165 170 175
 Asp Leu Gln Pro Pro Ser Ala Leu Ser Ala Pro Phe Thr Asn Ser Leu
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 Ala Arg Ser Ala Arg Gln Ser Val Leu Arg Tyr Ser Thr Leu Pro Gly
 195 200 205
 Arg Arg Ala Leu Lys Asn Ser Arg Leu Val Ser Gln Lys Asp Asp Val
 210 215 220
 His Val Cys Ile Leu Cys Leu Arg Ala Ile Met Asn Tyr Gln Tyr Gly
 225 230 235 240
 Phe Asn Leu Val Met Ser His Pro His Ala Val Asn Glu Ile Ala Leu
 245 250 255
 Ser Leu Asn Asn Lys Asn Pro Arg Thr Lys Ala Leu Val Leu Glu Leu
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 Leu Ala Ala Val Cys Leu Val Arg Gly Gly His Glu Ile Ile Leu Ala
 275 280 285
 Ala Phe Asp Asn Phe Lys Glu Val Cys Lys Glu Leu His Arg Phe Glu
 290 295 300
 Lys Leu Met Glu Tyr Phe Arg Asn Glu Asp Ser Asn Ile Asp Phe Met

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Met Asn Phe Arg Val His Leu Gln Tyr Glu Phe Thr Lys Leu Gly Leu			
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Glu Glu Phe Leu Gln Lys Ser Arg His Thr Glu Ser Glu Lys Leu Gln			
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Val Gln Ile Gln Ala Tyr Leu Asp Asn Val Phe Asp Val Gly Gly Leu			
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Leu Glu Asp Ala Glu Thr Lys Asn Val Ala Leu Glu Lys Val Glu Glu			
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Leu Glu Glu His Val Ser His Leu Thr Glu Lys Leu Leu Asp Leu Glu			
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Asn Glu Asn Met Met Arg Val Ala Glu Leu Glu Lys Gln Leu Leu Gln			
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Arg Glu Lys Glu Leu Glu Ser Ile Lys Glu Thr Tyr Glu Asn Thr Ser			
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His Gln Val His Thr Leu Arg Arg Leu Ile Lys Glu Lys Glu Glu Ala			
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Phe Gln Arg Arg Cys His Leu Glu Pro Asn Val Arg Gly Leu Glu Ser			
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Val Asp Ser Glu Ala Leu Ala Arg Val Gly Pro Ala Glu Leu Ser Glu			
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Glu Glu Val Leu Pro Leu Pro Pro Pro Ala Pro Pro Leu Pro Pro			
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Pro Pro Pro Pro Leu Pro Asp Lys Cys Pro Pro Ala Pro Pro Leu Pro			
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Gly Ala Ala Pro Ser Val Val Leu Thr Val Gly Leu Ser Ala Ile Arg			
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Ile Lys Lys Pro Ile Lys Thr Lys Phe Arg Leu Pro Val Phe Asn Trp			
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Thr Ala Leu Lys Pro Asn Gln Ile Ser Gly Thr Val Phe Ser Glu Leu			
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Asp Asp Glu Lys Ile Leu Glu Asp Leu Asp Leu Asp Lys Phe Glu Glu			
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Leu Phe Lys Thr Lys Ala Gln Gly Pro Ala Leu Asp Leu Ile Cys Ser			
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Lys Asn Lys Thr Ala Gln Lys Ala Ala Ser Lys Val Thr Leu Leu Glu			
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Ala Asn Arg Ala Lys Asn Leu Ala Ile Thr Leu Arg Lys Ala Gly Arg			
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Ser Ala Glu Glu Ile Cys Arg Ala Ile His Thr Phe Asp Leu Gln Thr			
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Leu Pro Val Asp Phe Val Glu Cys Leu Met Arg Phe Leu Pro Thr Glu			
675	680	685	
Ala Glu Val Lys Leu Leu Arg Gln Tyr Glu Arg Glu Arg Gln Pro Leu			
690	695	700	
Glu Glu Leu Ala Ala Glu Asp Arg Phe Met Leu Leu Phe Ser Lys Val			
705	710	715	720
Glu Arg Leu Thr Gln Arg Met Ala Gly Met Ala Phe Leu Gly Asn Phe			
725	730	735	
Gln Asp Asn Leu Gln Met Leu Thr Pro Gln Leu Asn Ala Ile Ile Ala			
740	745	750	
Ala Ser Ala Ser Val Lys Ser Ser Gln Lys Leu Lys Gln Met Leu Glu			
755	760	765	
Ile Ile Leu Ala Leu Gly Asn Tyr Met Asn Ser Ser Lys Arg Gly Ala			
770	775	780	
Val Tyr Gly Phe Lys Leu Gln Ser Leu Asp Leu Leu Leu Asp Thr Lys			
785	790	795	800

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 Lys Glu Lys Tyr Pro Asp Leu Ala Asn Phe Trp His Glu Leu His Phe
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 Val Glu Lys Ala Ala Ala Val Ser Leu Glu Asn Val Leu Leu Asp Val
 835 840 845
 Lys Glu Leu Gly Arg Gly Met Glu Leu Ile Arg Arg Glu Cys Ser Ile
 850 855 860
 His Asp Asn Ser Val Leu Arg Asn Phe Leu Ser Thr Asn Glu Gly Lys
 865 870 875 880
 Leu Asp Lys Leu Gln Arg Asp Ala Lys Thr Ala Glu Glu Ala Tyr Asn
 885 890 895
 Ala Val Val Arg Tyr Phe Gly Glu Ser Pro Lys Thr Thr Pro Pro Ser
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 Val Phe Phe Pro Val Phe Val Arg Phe Ile Arg Ser Tyr Lys Glu Ala
 915 920 925
 Glu Gln Glu Asn Glu Ala Arg Lys Lys Gln Glu Glu Val Met Arg Glu
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 Lys Gln Leu Ala Gln Glu Ala Lys Lys Leu Asp Ala Lys Thr Pro Ser
 945 950 955 960
 Gln Arg Asn Lys Trp Gln Gln Glu Leu Ile Ala Glu Leu Arg Arg
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 Arg Gln Ala Lys Glu His Arg Pro Val Tyr Glu Gly Lys Asp Gly Thr
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 Ile Glu Asp Ile Ile Thr Val Leu Lys Ser Val Pro Phe Thr Ala Arg
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<400> 237.

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 Tyr His Asn Phe Asp Arg Ser Arg His Asp Asp Asp Ile Arg Gly
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<213> Homo sapiens

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Glu Glu Asn Phe Arg Ser Asn Leu Arg Glu Val Ala Gln Met Leu Lys			
35	40	45	
Ser Lys His Gly Gly Asn Tyr Leu Leu Phe Asn Leu Ser Glu Arg Arg			
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Pro Asp Ile Thr Lys Leu His Ala Lys Val Leu Glu Phe Gly Trp Pro			
65	70	75	80
Asp Leu His Thr Pro Ala Leu Glu Lys Ile Cys Ser Ile Cys Lys Ala			
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Met Asp Thr Trp Leu Asn Ala Asp Pro His Asn Val Val Leu His			
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Asn Lys Gly Asn Arg Gly Arg Ile Gly Val Val Ile Ala Ala Tyr Met			
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His Tyr Ser Asn Ile Ser Ala Ser Ala Asp Gln Ala Leu Asp Arg Phe			
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Ala Met Lys Arg Phe Tyr Glu Asp Lys Ile Val Pro Ile Gly Gln Pro			
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Ser Gln Arg Arg Tyr Val His Tyr Phe Ser Gly Leu Leu Ser Gly Ser			
165	170	175	
Ile Lys Ile Asn Asn Lys Pro Leu Phe Leu His His Val Ile Met His			
180	185	190	
Gly Ile Pro Asn Phe Glu Ser Lys Gly Gly Cys Arg Pro Phe Leu Arg			
195	200	205	
Ile Tyr Gln Ala Met Gln Pro Val Tyr Thr Ser Gly Ile Tyr Asn Ile			
210	215	220	
Pro Gly Asp Ser Gln Thr Ser Val Cys Ile Thr Ile Glu Pro Gly Leu			
225	230	235	240
Leu Leu Lys Gly Asp Ile Leu Leu Lys Cys Tyr His Lys Lys Phe Arg			
245	250	255	
Ser Pro Ala Arg Asp Val Ile Phe Arg Val Gln Phe His Thr Cys Ala			
260	265	270	
Ile His Asp Leu Gly Val Val Phe Gly Lys Glu Asp Leu Asp Asp Ala			
275	280	285	
Phe Lys Asp Asp Arg Phe Pro Glu Tyr Gly Lys Val Glu Phe Val Phe			
290	295	300	
Ser Tyr Gly Pro Glu Lys Ile Gln Gly Met Glu His Leu Glu Asn Gly			
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Pro Ser Val Ser Val Asp Tyr Asn Thr Ser Asp Pro Leu Ile Arg Trp			
325	330	335	

Asp Ser Tyr Asp Asn Phe Ser Gly His Arg Asp Asp Gly Met Glu Glu
 340 345 350
 Val Val Gly His Thr Gln Gly Pro Leu Asp Gly Ser Leu Tyr Ala Lys
 355 360 365
 Val Lys Lys Lys Asp Ser Leu His Gly Ser Thr Gly Ala Val Asn Ala
 370 375 380
 Thr Arg Pro Thr Leu Ser Ala Thr Pro Asn His Val Glu His Thr Leu
 385 390 395 400
 Ser Val Ser Ser Asp Ser Gly Asn Ser Thr Ala Ser Thr Lys Thr Asp
 405 410 415
 Lys Thr Asp Glu Pro Val Pro Gly Ala Ser Ser Ala Thr Ala Ala Leu
 420 425 430
 Ser Pro Gln Glu Lys Arg Glu Leu Asp Arg Leu Leu Ser Gly Phe Gly
 435 440 445
 Leu Glu Arg Glu Lys Gln Gly Ala Met Tyr His Thr Gln His Leu Arg
 450 455 460
 Ser Arg Pro Ala Gly Gly Ser Ala Val Pro Ser Ser Gly Arg His Val
 465 470 475 480
 Val Pro Ala Gln Val His Val Asn Gly Gly Ala Leu Ala Ser Glu Arg
 485 490 495
 Glu Thr Asp Ile Leu Asp Asp Glu Leu Pro Asn Gln Asp Gly His Ser
 500 505 510
 Ala Gly Ser Met Gly Thr Leu Ser Ser Leu Asp Gly Val Thr Asn Thr
 515 520 525
 Ser Glu Gly Gly Tyr Pro Glu Ala Leu Ser Pro Leu Thr Asn Gly Leu
 530 535 540
 Asp Lys Ser Tyr Pro Met Glu Pro Met Val Asn Gly Gly Gly Tyr Pro
 545 550 555 560
 Tyr Glu Ser Ala Ser Arg Ala Gly Pro Ala His Ala Gly His Thr Ala
 565 570 575
 Pro Met Arg Pro Ser Tyr Ser Ala Gln Glu Gly Leu Ala Gly Tyr Gln
 580 585 590
 Arg Glu Gly Pro His Pro Ala Trp Pro Gln Pro Val Thr Thr Ser His
 595 600 605
 Tyr Ala His Asp Pro Ser Gly Met Phe Arg Ser Gln Ser Phe Ser Glu
 610 615 620
 Ala Glu Pro Gln Leu Pro Pro Ala Pro Val Arg Gly Gly Ser Ser Arg
 625 630 635 640
 Glu Ala Val Gln Arg Gly Leu Asn Ser Trp Gln Gln Gln Gln Gln
 645 650 655
 Gln Gln Gln Pro Arg Pro Pro Arg Gln Gln Glu Arg Ala His Leu
 660 665 670
 Glu Ser Leu Val Ala Ser Arg Pro Ser Pro Gln Pro Leu Ala Glu Thr
 675 680 685
 Pro Ile Pro Ser Leu Pro Glu Phe Pro Arg Ala Ala Ser Gln Gln Glu
 690 695 700
 Ile Glu Gln Ser Ile Glu Thr Leu Asn Met Leu Met Leu Asp Leu Glu
 705 710 715 720
 Pro Ala Ser Ala Ala Ala Pro Leu His Lys Ser Gln Ser Val Pro Gly
 725 730 735
 Ala Trp Pro Gly Ala Ser Pro Leu Ser Ser Gln Pro Leu Ser Gly Ser
 740 745 750
 Ser Arg Gln Ser His Pro Leu Thr Gln Ser Arg Ser Gly Tyr Ile Pro
 755 760 765
 Ser Gly His Ser Leu Gly Thr Pro Glu Pro Ala Pro Arg Ala Ser Leu
 770 775 780
 Glu Ser Val Pro Pro Gly Arg Ser Tyr Ser Pro Tyr Asp Tyr Gln Pro
 785 790 795 800
 Cys Leu Ala Gly Pro Asn Gln Asp Phe His Ser Lys Ser Pro Ala Ser
 805 810 815
 Ser Ser Leu Pro Ala Phe Leu Pro Thr Thr His Ser Pro Pro Gly Pro

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Gln	Gln	Pro	Pro	Ala	Ser	Leu	Pro	Gly	Leu	Thr	Ala	Gln	Pro	Leu	Leu
		835	840										845		
Ser	Pro	Lys	Glu	Ala	Thr	Ser	Asp	Pro	Ser	Arg	Thr	Pro	Glu	Glu	Glu
		850	855										860		
Pro	Leu	Asn	Leu	Glu	Gly	Leu	Val	Ala	His	Arg	Val	Ala	Gly	Val	Gln
		865	870										880		
Ala	Arg	Glu	Lys	Gln	Pro	Ala	Glu	Pro	Pro	Ala	Pro	Leu	Arg	Arg	Arg
													885	890	895
Ala	Ala	Ser	Asp	Gly	Gln	Tyr	Glu	Asn	Gln	Ser	Pro	Glu	Ala	Thr	Ser
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Pro	Arg	Ser	Pro	Gly	Val	Arg	Ser	Pro	Val	Gln	Cys	Val	Ser	Pro	Glu
													915	920	925
Leu	Ala	Leu	Thr	Ile	Ala	Leu	Asn	Pro	Gly	Gly	Arg	Pro	Lys	Glu	Pro
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His	Leu	His	Ser	Tyr	Lys	Glu	Ala	Phe	Glu	Glu	Met	Glu	Gly	Thr	Ser
													945	950	955
Pro	Ser	Ser	Pro	Pro	Ser	Gly	Val	Arg	Ser	Pro	Pro	Gly	Leu	Ala	
													965	970	975
Lys	Thr	Pro	Leu	Ser	Ala	Leu	Gly	Leu	Lys	Pro	His	Asn	Pro	Ala	Asp
													980	985	990
Ile	Leu	Leu	His	Pro	Thr	Gly	Val	Thr	Arg	Arg	Ile	Gln	Pro	Glu	
													995	1000	1005
Glu	Asp	Glu	Gly	Lys	Val	Val	Val	Arg	Leu	Ser	Glu	Glu	Pro	Arg	Ser
													1010	1015	1020
Tyr	Val	Glu	Ser	Val	Ala	Arg	Thr	Ala	Val	Ala	Gly	Pro	Arg	Ala	Gln
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Asp	Ser	Glu	Pro	Lys	Ser	Phe	Ser	Ala	Pro	Ala	Thr	Gln	Ala	Tyr	Gly
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His	Glu	Ile	Pro	Leu	Arg	Asn	Gly	Thr	Leu	Gly	Gly	Ser	Phe	Val	Ser
													1060	1065	1070
Pro	Ser	Pro	Leu	Ser	Thr	Ser	Pro	Ile	Leu	Ser	Ala	Asp	Ser	Thr	
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Ser	Val	Gly	Ser	Phe	Pro	Ser	Gly	Glu	Ser	Ser	Asp	Gln	Gly	Pro	Arg
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Thr	Pro	Thr	Gln	Pro	Leu	Leu	Glu	Ser	Gly	Phe	Arg	Ser	Gly	Ser	Leu
													1105	1110	1115
Gly	Gln	Pro	Ser	Pro	Ser	Ala	Gln	Arg	Asn	Tyr	Gln	Ser	Ser	Pro	
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Leu	Pro	Thr	Val	Gly	Ser	Ser	Tyr	Ser	Ser	Pro	Asp	Tyr	Ser	Leu	Gln
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His	Phe	Ser	Ser	Pro	Glu	Ser	Gln	Ala	Arg	Ala	Gln	Phe	Ser	Val	
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Ala	Gly	Val	His	Thr	Val	Pro	Gly	Ser	Pro	Gln	Ala	Arg	His	Arg	Thr
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Val	Gly	Thr	Asn	Thr	Pro	Pro	Ser	Pro	Gly	Phe	Gly	Arg	Arg	Ala	Ile
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Asn	Pro	Ser	Met	Ala	Ala	Pro	Ser	Ser	Pro	Ser	Leu	Ser	His	His	Gln
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Met	Met	Gly	Pro	Pro	Gly	Thr	Gly	Phe	His	Gly	Ser	Thr	Val	Ser	Ser
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Pro	Gln	Ser	Ser	Ala	Ala	Thr	Thr	Pro	Gly	Ser	Pro	Ser	Leu	Cys	Arg
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Thr	Thr	Pro	Gly	Ser	Pro	Ser	Leu	Gly	Arg	His	Pro	Gly	Ala	His	Gln
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Gly	Asn	Leu	Ala	Ser	Gly	Leu	His	Ser	Asn	Ala	Ile	Ala	Ser	Pro	Gly
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Ser	Pro	Ser	Leu	Gly	Arg	His	Leu	Gly	Gly	Ser	Gly	Ser	Val	Val	Pro
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 Phe Arg Gln Gly Ser Pro Thr Pro Ala Leu Pro Glu Lys Arg Arg Met
 1380 1385 1390
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 1410 1415 1420
 Gly Ser Thr Val Ser Phe Ser His Thr Leu Pro Asp Phe Ser Lys Tyr
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 Ser Met Pro Asp Asn Ser Pro Glu Thr Arg Ala Lys Val Lys Phe Val
 1445 1450 1455
 Gln Asp Thr Ser Lys Tyr Trp Tyr Lys Pro Glu Ile Ser Arg Glu Gln
 1460 1465 1470
 Ala Ile Ala Leu Leu Lys Asp Gln Glu Pro Gly Ala Phe Ile Ile Arg
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 Gln Gly Ser Thr Thr Cys His Leu Phe Ala Glu Leu Asp Pro Asn Gln
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<211> 3557

<212> DNA

<213> Homo sapiens

<400> 241

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 35 40 45
 Ala Ala Ala Phe Leu Gly Asp Ile Ala Leu Asp Glu Glu Asp Leu Arg
 50 55 60
 Ala Phe Gln Val Gln Gln Ala Val Asp Leu Arg Arg His Thr Ala Arg
 65 70 75 80
 Lys Ser Ser Ile Lys Ala Ala Val Pro Gly Asn Thr Ser Thr Pro Ser
 85 90 95
 Cys Gln Ser Thr Asn Gly Gln Pro Gln Arg Gly Ala Cys Gly Arg Trp
 100 105 110
 Arg Gly Arg Ser Arg Ser Arg Arg Ala Ala Thr Ser Arg Pro Glu Arg
 115 120 125
 Val Trp Pro Asp Gly Val Ile Pro Phe Val Ile Gly Gly Asn Phe Thr
 130 135 140
 Gly Ser Gln Arg Ala Val Phe Arg Gln Ala Met Arg His Trp Glu Lys
 145 150 155 160
 His Thr Cys Val Thr Phe Leu Glu Arg Thr Asp Glu Asp Ser Tyr Ile
 165 170 175
 Val Phe Thr Tyr Arg Pro Cys Gly Cys Ser Tyr Val Gly Arg Arg
 180 185 190
 Gly Gly Gly Pro Gln Ala Ile Ser Ile Gly Lys Asn Cys Asp Lys Phe
 195 200 205
 Gly Ile Val Val His Glu Leu Gly His Val Val Gly Phe Trp His Glu
 210 215 220
 His Thr Arg Pro Asp Arg Asp Arg His Val Ser Ile Val Arg Glu Asn
 225 230 235 240
 Ile Gln Pro Gly Gln Glu Tyr Asn Phe Leu Lys Met Glu Pro Gln Glu
 245 250 255
 Val Glu Ser Leu Gly Glu Thr Tyr Asp Phe Asp Ser Ile Met His Tyr
 260 265 270
 Ala Arg Asn Thr Phe Ser Arg Gly Ile Phe Leu Asp Thr Ile Val Pro
 275 280 285
 Lys Tyr Glu Val Asn Gly Val Lys Pro Pro Ile Gly Gln Arg Thr Arg
 290 295 300
 Leu Ser Lys Gly Asp Ile Ala Gln Ala Arg Lys Leu Tyr Lys Cys Pro
 305 310 315 320
 Ala Cys Gly Glu Thr Leu Gln Asp Ser Thr Gly Asn Phe Ser Ser Pro
 325 330 335
 Glu Tyr Pro Asn Gly Tyr Ser Ala His Met His Cys Val Trp Arg Ile
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 Ser Val Thr Pro Gly Glu Lys Ile Ile Leu Asn Phe Thr Ser Leu Asp
 355 360 365
 Leu Tyr Arg Ser Arg Leu Cys Trp Tyr Asp Tyr Val Glu Val Arg Asp
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 385 390 395 400
 Leu Pro Glu Pro Ile Val Ser Thr Asp Ser Arg Leu Trp Val Glu Phe
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 Arg Ser Ser Ser Asn Trp Val Gly Lys Gly Phe Phe Ala Val Tyr Glu
 420 425 430
 Ala Ile Cys Gly Gly Asp Val Lys Lys Asp Tyr Gly His Ile Gln Ser

435	440	445
Pro Asn Tyr Pro Asp Asp Tyr Arg Pro Ser Lys Val Cys Ile Trp Arg		
450	455	460
Ile Gln Val Ser Glu Gly Phe His Val Gly Leu Thr Phe Gln Ser Phe		
465	470	475
Glu Ile Glu Arg His Asp Ser Cys Ala Tyr Asp Tyr Leu Glu Val Arg		
485	490	495
Asp Gly His Ser Glu Ser Ser Thr Leu Ile Gly Arg Tyr Cys Gly Tyr		
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Glu Lys Pro Asp Asp Ile Lys Ser Thr Ser Ser Arg Leu Trp Leu Lys		
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Phe Val Ser Asp Gly Ser Ile Asn Lys Ala Gly Phe Ala Val Asn Phe		
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Phe Lys Glu Val Asp Glu Cys Ser Arg Pro Asn Arg Gly Gly Cys Glu		
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Gln Arg Cys Leu Asn Thr Leu Gly Ser Tyr Lys Cys Ser Cys Asp Pro		
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Gly Phe Leu Thr Lys Leu Asn Gly Ser Ile Thr Ser Pro Gly Trp Pro		
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Lys Glu Tyr Pro Pro Asn Lys Asn Cys Ile Trp Gln Leu Val Ala Pro		
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Asn Asp Val Cys Lys Tyr Asp Phe Val Glu Val Arg Ser Gly Leu Thr		
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Ala Asp Ser Lys Leu His Gly Lys Phe Cys Gly Ser Glu Lys Pro Glu		
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Val Ile Thr Ser Gln Tyr Asn Asn Met Arg Val Glu Phe Lys Ser Asp		
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Asp Asn Lys His Asp Cys Lys Glu Ala Gly Cys Asp His Lys Val Thr		
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Ser Thr Ser Gly Thr Ile Thr Ser Pro Asn Trp Pro Asp Lys Tyr Pro		
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Val Lys Leu Thr Phe Met Glu Met Asp Ile Glu Ser Gln Pro Glu Cys		
785	790	795
800		
Ala Tyr Asp His Leu Glu Val Phe Asp Gly Arg Asp Ala Lys Ala Pro		
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Val Leu Gly Arg Phe Cys Gly Ser Lys Lys Pro Glu Pro Val Leu Ala		
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Arg Lys Gly Phe Gln Ala Ser His Ala Thr Glu Cys Gly Gly Gln Val		
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Arg Ala Asp Val Lys Thr Lys Asp Leu Tyr Ser His Ala Gln Phe Gly		
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<212> DNA

<213> Homo sapiens

<400> 243

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 Phe Gln Ser Thr Pro Lys Leu Thr Arg Leu Asp Leu Ser Glu Asn Gln
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 Phe Arg Ala Leu Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn
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 Thr Leu Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala
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 Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp Val
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 Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro Pro Ser
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 Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr Cys Ser Asn
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Trp Leu Gly Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro		
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Arg Cys Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val		
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Ala Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln		
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His Ala Phe Asn Gly Leu Arg Ser Leu Arg Val Leu Thr Leu His Gly		
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<210> 246

<211> 818

<212> PRT

<213> Homo sapiens

<400> 246

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Arg	Ser	Lys	Lys	Leu	Pro	Leu	Thr	Thr	Leu	Ala	Gln	Cys	Leu	Met	Glu
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Cys	Arg	Asp	Gln	Leu	Ser	Ala	Asp	Met	Tyr	Ser	Phe	Val	Ala	Lys	Glu
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Ile	Asp	Tyr	Ala	Asn	Tyr	Phe	Gln	Thr	Leu	Ile	Glu	Val	Gln	Ala	Glu
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Tyr	His	Arg	Lys	Ser	Leu	Thr	Leu	Leu	Gln	Ala	Val	Leu	Pro	Gln	Ile
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Lys	Ala	Gln	Gln	Glu	Ala	Trp	Val	Glu	Lys	Pro	Ser	Phe	Gly	Lys	Pro
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Leu	Glu	Glu	His	Leu	Thr	Ile	Ser	Gly	Arg	Glu	Ile	Ala	Phe	Pro	Ile
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Glu	Ala	Cys	Val	Thr	Met	Leu	Leu	Glu	Cys	Gly	Met	Gln	Glu	Glu	Gly
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Leu	Phe	Arg	Val	Ala	Pro	Ser	Ala	Ser	Lys	Leu	Lys	Lys	Leu	Lys	Ala
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Ala	Leu	Asp	Cys	Cys	Val	Val	Asp	Val	Gln	Glu	Tyr	Ser	Ala	Asp	Pro
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His	Ala	Ile	Ala	Gly	Ala	Leu	Lys	Ser	Tyr	Leu	Arg	Glu	Leu	Pro	Glu
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 Lys Leu Pro Lys Ala Asn His Asn Asn Ile Arg Tyr Leu Ile Lys Phe
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 Leu Ser Lys Leu Ser Glu Tyr Gln Asp Val Asn Lys Met Thr Pro Ser
 385 390 395 400
 Asn Met Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Pro Gln Ala Glu
 405 410 415
 Gly Asn Ile Thr Glu Met Met Thr Thr Val Ser Leu Gln Ile Val Gly
 420 425 430
 Ile Ile Glu Pro Ile Ile Gln His Ala Asp Trp Phe Phe Pro Gly Glu
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 His Asn Ala Asn Tyr Ser Ser Met Pro Ser Pro Asp Met Asp Pro Ala
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 Asp Arg Arg Gln Pro Glu Gln Ala Arg Arg Pro Leu Ser Val Ala Thr
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 Asp Asn Met Met Leu Glu Phe Tyr Lys Asp Gly Leu Arg Lys Ile
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 Gln Ser Met Gly Val Arg Val Met Asp Thr Asn Trp Val Ala Arg Arg
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 Gly Ser Ser Ala Gly Arg Lys Val Ser Cys Ala Pro Pro Ser Met Gln
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 Pro Glu Gln Pro Leu Asp Ser Pro Ala Ala Pro Ala Leu Ser Pro Ser
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 Gly Leu Gly Leu Gln Pro Gly Pro Glu Arg Thr Ser Thr Thr Lys Ser
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 Lys Glu Leu Ser Pro Gly Ser Ala Gln Lys Gly Ser Pro Gly Ser Ser
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 Gln Gly Thr Ala Cys Ala Gly Thr Gln Pro Gly Ala Gln Pro Gly Ala
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 Gln Pro Gly Ala Ser Pro Ser Pro Ser Gln Pro Pro Ala Asp Gln Ser
 625 630 635 640
 Pro His Thr Leu Arg Lys Val Ser Lys Lys Leu Ala Pro Ile Pro Pro
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 Lys Val Pro Phe Gly Gln Pro Gly Ala Met Ala Asp Gln Ser Ala Gly
 660 665 670
 Gln Leu Ser Pro Val Ser Leu Ser Pro Thr Pro Pro Ser Thr Pro Ser
 675 680 685
 Pro Tyr Gly Leu Ser Tyr Pro Gln Gly Tyr Ser Leu Ala Ser Gly Gln
 690 695 700
 Leu Ser Pro Ala Ala Ala Pro Pro Leu Ala Ser Pro Ser Val Phe Thr
 705 710 715 720
 Ser Thr Leu Ser Lys Ser Arg Pro Thr Pro Lys Pro Arg Gln Arg Pro
 725 730 735
 Thr Leu Pro Pro Gln Pro Pro Thr Val Asn Leu Ser Ala Ser Ser
 740 745 750
 Pro Gln Ser Thr Glu Ala Pro Met Leu Asp Gly Met Ser Pro Gly Glu
 755 760 765
 Ser Met Ser Thr Asp Leu Val His Phe Asp Ile Pro Ser Ile His Ile
 770 775 780
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Ala Leu

<210> 247
 <211> 2850
 <212> DNA
 <213> Homo sapiens

<400> 247

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 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 248

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 Cys Glu Val Thr Tyr Asp Lys Thr Pro Leu Glu Lys Asp Gly Ile Thr
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 Val Val Asp Trp Pro Phe Asp Asp Gly Ala Pro Pro Pro Gly Lys Val
 65 70 75 80
 Val Glu Asp Trp Leu Ser Leu Val Lys Ala Lys Phe Cys Glu Ala Pro
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 Gly Ser Cys Val Ala Val His Cys Val Ala Gly Leu Gly Arg Ala Pro
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 Val Leu Val Ala Leu Ala Ile Glu Ser Gly Met Lys Tyr Glu Asp
 115 120 125
 Ala Ile Gln Phe Ile Arg Gln Lys Arg Arg Gly Ala Ile Asn Ser Lys
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<210> 249

<211> 3853

<212> DNA

<213> Homo sapiens

<400> 249

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<210> 250
 <211> 1179
 <212> PRT
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<400> 250
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 Val Lys Asn Ser Met Thr Phe Ser Gly Pro Val Glu Asp Met Phe Gly
 35 40 45
 Tyr Thr Val Gln Gln Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile
 50 55 60
 Gly Ser Pro Leu Val Gly Gln Pro Lys Asn Arg Thr Gly Asp Val Tyr
 65 70 75 80
 Lys Cys Pro Val Gly Arg Gly Glu Ser Leu Pro Cys Val Lys Leu Asp
 85 90 95
 Leu Pro Val Asn Thr Ser Ile Pro Asn Val Thr Glu Val Lys Glu Asn
 100 105 110
 Met Thr Phe Gly Ser Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu
 115 120 125
 Ala Cys Gly Pro Leu Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr
 130 135 140
 Thr Gly Ile Cys Ser Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser

145	150	155	160
Ile Ala Pro Val Gln Glu Cys Ser Thr Gln	Leu Asp Ile Val Ile Val		
165	170	175	
Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Asp Ser Val Thr Ala Phe			
180	185	190	
Leu Asn Asp Leu Leu Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln			
195	200	205	
Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu			
210	215	220	
Asn Lys Tyr Ser Ser Thr Glu Glu Val Leu Val Ala Ala Lys Lys Ile			
225	230	235	240
Val Gln Arg Gly Arg Gln Thr Met Thr Ala Leu Gly Thr Asp Thr			
245	250	255	
Ala Arg Lys Glu Ala Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val			
260	265	270	
Lys Lys Val Met Val Ile Val Thr Asp Gly Glu Ser His Asp Asn His			
275	280	285	
Arg Leu Lys Lys Val Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg			
290	295	300	
Phe Ser Ile Ala Ile Leu Gly Ser Tyr Asn Arg Gly Asn Leu Ser Thr			
305	310	315	320
Glu Lys Phe Val Glu Glu Ile Lys Ser Ile Ala Ser Glu Pro Thr Glu			
325	330	335	
Lys His Phe Asn Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val			
340	345	350	
Lys Thr Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln			
355	360	365	
Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala			
370	375	380	
His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp			
385	390	395	400
Trp Asn Gly Thr Val Val Met Gln Lys Ala Ser Gln Ile Ile Ile Pro			
405	410	415	
Arg Asn Thr Thr Phe Asn Val Glu Ser Thr Lys Lys Asn Glu Pro Leu			
420	425	430	
Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr Ala Ser Ser Gly			
435	440	445	
Asp Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln			
450	455	460	
Val Ile Ile Tyr Arg Met Glu Asp Gly Asn Ile Lys Ile Leu Gln Thr			
465	470	475	480
Leu Ser Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Ile Leu Thr Thr			
485	490	495	
Thr Asp Ile Asp Lys Asp Ser Asn Thr Asp Ile Leu Leu Val Gly Ala			
500	505	510	
Pro Met Tyr Met Gly Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val			
515	520	525	
Tyr Ala Leu Asn Gln Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro			
530	535	540	
Ile Lys Gln Thr Cys Cys Ser Ser Arg Gln His Asn Ser Cys Thr Thr			
545	550	555	560
Glu Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala			
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Ala Val Lys Asp Leu Asn Leu Asp Gly Phe Asn Asp Ile Val Ile Gly			
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Ala Pro Leu Glu Asp Asp His Gly Gly Ala Val Tyr Ile Tyr His Gly			
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Ser Gly Lys Thr Ile Arg Lys Glu Tyr Ala Gln Arg Ile Pro Ser Gly			
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Gly Asp Gly Lys Thr Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu			
625	630	635	640

Met Asp Leu Asn Gly Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu
 645 650 655
 Gly Gly Ala Ala Leu Phe Trp Ser Arg Asp Val Ala Val Val Lys Val
 660 665 670
 Thr Met Asn Phe Glu Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys
 675 680 685
 His Met Glu Gly Lys Glu Thr Val Cys Ile Asn Ala Thr Val Cys Phe
 690 695 700
 Glu Val Lys Leu Lys Ser Lys Glu Asp Thr Ile Tyr Glu Ala Asp Leu
 705 710 715 720
 Gln Tyr Arg Val Thr Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe
 725 730 735
 Phe Ser Gly Thr Gln Glu Arg Lys Val Gln Arg Asn Ile Thr Val Arg
 740 745 750
 Lys Ser Glu Cys Thr Lys His Ser Phe Tyr Met Leu Asp Lys His Asp
 755 760 765
 Phe Gln Asp Ser Val Arg Ile Thr Leu Asp Phe Asn Leu Thr Asp Pro
 770 775 780
 Glu Asn Gly Pro Val Leu Asp Asp Ser Leu Pro Asn Ser Val His Glu
 785 790 795 800
 Tyr Ile Pro Phe Ala Lys Asp Cys Gly Asn Lys Glu Lys Cys Ile Ser
 805 810 815
 Asp Leu Ser Leu His Val Ala Thr Thr Glu Lys Asp Leu Leu Ile Val
 820 825 830
 Arg Ser Gln Asn Asp Lys Phe Asn Val Ser Leu Thr Val Lys Asn Thr
 835 840 845
 Lys Asp Ser Ala Tyr Asn Thr Arg Thr Ile Val His Tyr Ser Pro Asn
 850 855 860
 Leu Val Phe Ser Gly Ile Glu Ala Ile Gln Lys Asp Ser Cys Glu Ser
 865 870 875 880
 Asn His Asn Ile Thr Cys Lys Val Gly Tyr Pro Phe Leu Arg Arg Gly
 885 890 895
 Glu Met Val Thr Phe Lys Ile Leu Phe Gln Phe Asn Thr Ser Tyr Leu
 900 905 910
 Met Glu Asn Val Thr Ile Tyr Leu Ser Ala Thr Ser Asp Ser Glu Glu
 915 920 925
 Pro Pro Glu Thr Leu Ser Asp Asn Val Val Asn Ile Ser Ile Pro Val
 930 935 940
 Lys Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu Tyr His
 945 950 955 960
 Ile Ser Ile Ala Ala Asn Glu Thr Val Pro Glu Val Ile Asn Ser Thr
 965 970 975
 Glu Asp Ile Gly Asn Glu Ile Asn Ile Phe Tyr Leu Ile Arg Lys Ser
 980 985 990
 Gly Ser Phe Pro Met Pro Glu Leu Lys Leu Ser Ile Ser Phe Pro Asn
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 Met Thr Ser Asn Gly Tyr Pro Val Leu Tyr Pro Thr Gly Leu Ser Ser
 1010 1015 1020
 Ser Glu Asn Ala Asn Cys Arg Pro His Ile Phe Glu Asp Pro Phe Ser
 1025 1030 1035 1040
 Ile Asn Ser Gly Lys Lys Met Thr Thr Ser Thr Asp His Leu Lys Arg
 1045 1050 1055
 Gly Thr Ile Leu Asp Cys Asn Thr Cys Lys Phe Ala Thr Ile Thr Cys
 1060 1065 1070
 Asn Leu Thr Ser Ser Asp Ile Ser Gln Val Asn Val Ser Leu Ile Leu
 1075 1080 1085
 Trp Lys Pro Thr Phe Ile Lys Ser Tyr Phe Ser Ser Leu Asn Leu Thr
 1090 1095 1100
 Ile Arg Gly Glu Leu Arg Ser Glu Asn Ala Ser Leu Val Leu Ser Ser
 1105 1110 1115 1120
 Ser Asn Gln Lys Arg Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly Leu

	1125	1130	1135												
Pro	Gly	Arg	Val	Pro	Leu	Trp	Val	Ile	Leu	Leu	Ser	Ala	Phe	Ala	Gly
				1140			1145					1150			
Leu	Leu	Leu	Leu	Met	Leu	Leu	Ile	Leu	Ala	Leu	Trp	Lys	Ile	Gly	Phe
				1155			1160				1165				
Phe	Lys	Arg	Pro	Leu	Lys	Lys	Lys	Met	Glu	Lys					
				1170			1175								

<210> 251

<211> 5010

<212> DNA

<213> Homo sapiens

<400> 251

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tgccatggag	tgaagggaca	aaagggtgaa	agaggcctcc	cggggttaca	aggtgtcatt	180
gggtttctg	gaatgcagg	acctgagggg	ccacaggac	caccaggaca	aaagggtgat	240
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ggtattccag	gatgcattgg	cacAAAGGGG	gagagaggc	cgctcgggccc	tcctggcttg	420
cctggtttcg	caggAAATCC	cgggaccacca	ggcttaccag	ggatgaaggg	tgatccagg	480
gagatacttg	gcattgtgcc	cgggatgtct	ttggAAAGGT	aaagaggatt	tcccggaaatc	540
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acctgcaatt	actacgcaaa	cgcttacagc	tttggctcg	ccaccataga	gaggagcggag	4920
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<210> 252
<211> 1669
<212> PRT
<213> *Homo sapiens*

<400> 252

Met	Gly	Pro	Arg	Leu	Ser	Val	Trp	Leu	Leu	Leu	Leu	Pro	Ala	Ala	Leu
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Leu	Leu	His	Glu	Glu	His	Ser	Arg	Ala	Ala	Ala	Lys	Gly	Gly	Cys	Ala
					20				25				30		
Gly	Ser	Gly	Cys	Gly	Lys	Cys	Asp	Cys	His	Gly	Val	Lys	Gly	Gln	Lys
					35			40				45			
Gly	Glu	Arg	Gly	Leu	Pro	Gly	Leu	Gln	Gly	Val	Ile	Gly	Phe	Pro	Gly
					50			55			60				
Met	Gln	Gly	Pro	Glu	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Gln	Lys	Gly	Asp
					65			70			75			80	
Thr	Gly	Glu	Pro	Gly	Leu	Pro	Gly	Thr	Lys	Gly	Thr	Arg	Gly	Pro	Pro
						85			90			95			
Gly	Ala	Ser	Gly	Tyr	Pro	Gly	Asn	Pro	Gly	Leu	Pro	Gly	Ile	Pro	Gly
					100				105				110		
Gln	Asp	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ile	Pro	Gly	Cys	Asn	Gly	Thr

115	120	125
Lys	Gly	Glu Arg Gly Pro Leu
130	135	140
Gly	Asn Pro Gly Pro Pro Gly	Leu Pro Gly Met Lys
145	150	155
Glu	Ile Leu Gly His Val Pro Gly	Met Leu Leu Lys
165	170	175
Phe	Pro Gly Ile Pro Gly Thr	Pro Pro Gly Leu Pro
180	185	190
Gln	Gly Pro Val Gly Pro Pro Gly	Phe Thr Gly Pro Pro
195	200	205
Gly	Pro Pro Gly Pro Pro Gly	Glu Lys Gly Gln Met
210	215	Gly Leu Ser Phe
Gln	Gly Pro Lys Gly Asp Lys	Gly Val Ser Gly Pro
225	230	235
Gly	Val Pro Gly Gln Ala Gln	Val Gln Glu Lys Gly
245	250	Asp Phe Ala Thr
Lys	Gly Glu Lys Gly Gln Lys	Gly Phe Gln Gly Met
260	265	Pro Pro Gly
Gly	Val Gly Glu Lys Gly Glu	Gly Lys Pro Arg Gly
275	280	Lys 285
Pro	Gly Lys Asp Gly Asp Lys	Gly Ser Pro Gly Phe
290	295	Pro Pro
Gly	Glu Pro Gly Tyr Pro Gly	Leu Ile Gly Arg Gln
305	310	Gly Pro Gln Gly
Glu	Lys Gly Glu Ala Gly Pro	Pro Pro Gly Ile Val
325	330	Ile Gly 335
Thr	Gly Pro Leu Gly Glu Lys	Gly Arg Gly Tyr Pro
340	345	Gly Thr Pro
Gly	Pro Arg Gly Glu Pro Gly	Pro Lys Gly Phe Pro
355	360	Gly Leu Pro Gly
Gln	Pro Gly Pro Pro Gly	Leu Pro Val Pro Gly
370	375	Gln Ala Gly Ala Pro
Gly	Phe Pro Gly Glu Arg Gly	Glu Lys Gly Asp Arg
385	390	Gly Phe Pro Gly
Thr	Ser Leu Pro Gly Pro Ser	Gly Arg Asp Gly Leu
405	410	Pro Pro Gly
Gly	Ser Pro Gly Pro Pro Gly	Gln Pro Gly Tyr Thr
420	425	Asn Gly Ile Val
Glu	Cys Gln Pro Gly Pro Pro	Gly Phe Pro Gly Ile
435	440	Pro Pro Gly
Gly	Gln Pro Gly Phe Ile	Gly Glu Ile Gly Glu
450	455	Lys Gly Gln Lys Gly
Glu	Ser Cys Leu Ile Cys Asp	Ile Asp Gly Tyr Arg
465	470	Gly Pro Pro Gly
Pro	Gln Gly Pro Pro Gly Glu	Ile Gly Phe Pro Gly
485	490	Gln Pro Gly Ala
Lys	Gly Asp Arg Gly Leu	Gly Val Ala Gly Val
500	505	Pro
Gly	Pro Gln Gly Thr Pro	Gly Arg Asp Gly Val
515	520	Gly Ala Lys Gly
Glu	Pro Gly Glu Phe Tyr	Phe Asp Leu Arg Leu
530	535	Lys Gly Asp Lys Gly
Asp	Pro Gly Phe Pro Gly	Gln Pro Gly Met Pro
545	550	Gly Arg Ala Gly Ser
Pro	Gly Arg Asp Gly His	Pro Gly Pro Lys Gly
565	570	Ser Pro
Gly	Ser Val Gly Leu Lys	Gly Glu Arg Gly Pro
580	585	Pro Pro Gly Val Gly
Phe	Pro Gly Ser Arg Gly Asp	Thr Gly Pro Pro Gly
595	600	Pro Pro Gly Tyr
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Gly Pro Ala Gly Pro Ile Gly Asp Lys Gly Gln Ala Gly Phe Pro Gly
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 Gly Pro Gly Ser Pro Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly Lys
 625 630 635 640
 Ile Val Pro Leu Pro Gly Pro Pro Gly Ala Glu Gly Leu Pro Gly Ser
 645 650 655
 Pro Gly Phe Pro Gly Pro Gln Gly Asp Arg Gly Phe Pro Gly Thr Pro
 660 665 670
 Gly Arg Pro Gly Leu Pro Gly Glu Lys Gly Ala Val Gly Gln Pro Gly
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 740 745 750
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 His Gly Ala Ile Gly Pro Pro Gly Leu Gln Gly Ile Arg Gly Glu Pro
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 Phe Pro Gly Leu Asp Met Pro Gly Pro Lys Gly Asp Lys Gly Ala Gln
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 Gln Gln Gly Ala Pro Gly Ile Pro Gly Phe Pro Gly Ser Lys Gly Glu
 865 870 875 880
 Met Gly Val Met Gly Thr Pro Gly Gln Pro Gly Ser Pro Gly Pro Val
 885 890 895
 Gly Ala Pro Gly Leu Pro Gly Glu Lys Gly Asp His Gly Phe Pro Gly
 900 905 910
 Ser Ser Gly Pro Arg Gly Asp Pro Gly Leu Lys Gly Asp Lys Gly Asp
 915 920 925
 Val Gly Leu Pro Gly Lys Pro Gly Ser Met Asp Lys Val Asp Met Gly
 930 935 940
 Ser Met Lys Gly Gln Lys Gly Asp Gln Gly Glu Lys Gly Gln Ile Gly
 945 950 955 960
 Pro Ile Gly Glu Lys Gly Ser Arg Gly Asp Pro Gly Thr Pro Gly Val
 965 970 975
 Pro Gly Lys Asp Gly Gln Ala Gly Gln Pro Gly Gln Pro Gly Pro Lys
 980 985 990
 Gly Asp Pro Gly Ile Ser Gly Thr Pro Gly Ala Pro Gly Leu Pro Gly
 995 1000 1005
 Pro Lys Gly Ser Val Gly Gly Met Gly Leu Pro Gly Thr Pro Gly Glu
 1010 1015 1020
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 Gly Asp Lys Gly Ala Lys Gly Glu Lys Gly Gln Ala Gly Pro Pro Gly
 1045 1050 1055
 Ile Gly Ile Pro Gly Leu Arg Gly Glu Lys Gly Asp Gln Gly Ile Ala
 1060 1065 1070
 Gly Phe Pro Gly Ser Pro Gly Glu Lys Gly Glu Lys Gly Ser Ile Gly
 1075 1080 1085
 Ile Pro Gly Met Pro Gly Ser Pro Gly Leu Lys Gly Ser Pro Gly Ser

1090	1095	1100
Val	Gly	Tyr
Pro	Gly	Ser
Pro	Gly	Leu
Pro	Gly	Pro
Gly	Asp	Gly
Ile	Pro	Gly
Val	Lys	Gly
Glu	Gly	Asp
Lys	Gly	Lys
1105	1110	1115
Gly	Leu	Pro
Gly	Leu	Asp
Gly	Ile	Pro
1125	1130	1135
Leu	Pro	Gly
Thr	Pro	Gly
Pro	Thr	Gly
Gly	Pro	Ala
1140	1145	1150
Pro	Gly	Ser
Asp	Gly	Ile
Pro	Gly	Ser
Ala	Gly	Glu
Glu	Lys	Gly
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Gly	Arg	Gly
Phe	Pro	Gly
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Gly	Ala	Lys
Gly	Asp	
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Lys	Gly	Glu
Val	Gly	Phe
Pro	Gly	Leu
Ala	Gly	Ser
Pro	1185	1190
Gly	Ile	Pro
Ser	Lys	Gly
Glu	Gln	Gly
Phe	Met	Gly
Pro	Pro	Gly
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Gln	Pro	Gly
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Ser	Pro	Gly
His	Ala	Thr
Glu	1220	1225
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Lys	Gly	Asp
Arg	Gly	Pro
Gln	Gly	Gln
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 <212> DNA
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 Gly Val Ala Ile Asp Thr Val Glu Asp Thr Lys Ile Leu Phe Asp Gly
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 180 185 190
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 225 230 235 240
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 Asn Ser Ile Ser Ile Ser Gly Tyr His Met Gln Glu Ala Gly Ala Asp
 260 265 270
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 Lys Met Arg Ala Gly Arg Arg Leu Trp Ala His Leu Ile Glu Lys Met
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 Phe Gln Pro Lys Asn Ser Lys Ser Leu Leu Leu Arg Ala His Cys Gln
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 Thr Ser Gly Trp Ser Leu Thr Glu Gln Asp Pro Tyr Asn Asn Ile Val
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Cys Leu Thr Asn Asp Val Tyr Asp Ala Ala Leu Lys Leu Ile Asn Glu			
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Lys Ala Asn Asp Arg Met Val Ser Gly Ala Tyr Arg Gln Glu Phe Gly			
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Glu Arg Glu Gly Arg Arg Pro Arg Leu Leu Val Ala Lys Met Gly Gln			
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 <211> 3063
 <212> PRT
 <213> Homo sapiens

<400> 257

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Leu	Leu	Ser	Ser	Ile	Glu	Ala	Glu	Val	Asp	Pro	Pro	Ser	Asp	Leu	Asn
					20			25						30	
Phe	Lys	Ile	Ile	Asp	Glu	Asn	Thr	Val	His	Met	Ser	Trp	Ala	Glu	Pro
						35		40						45	
Val	Asp	Pro	Ile	Val	Gly	Tyr	Arg	Ile	Thr	Val	Asp	Pro	Thr	Thr	Asp
				50				55						60	

Gly Pro Thr Lys Glu Phe Thr Leu Ser Ala Ser Thr Thr Glu Thr Leu
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 Leu Ser Glu Leu Val Pro Glu Thr Glu Tyr Val Val Thr Ile Thr Ser
 85 90 95
 Tyr Asp Glu Val Glu Glu Ser Val Pro Val Ile Gly Gln Leu Thr Ile
 100 105 110
 Gln Thr Gly Ser Ser Thr Lys Pro Val Glu Lys Lys Pro Gly Lys Thr
 115 120 125
 Glu Ile Gln Lys Cys Ser Val Ser Ala Trp Thr Asp Leu Val Phe Leu
 130 135 140
 Val Asp Gly Ser Trp Ser Val Gly Arg Asn Asn Phe Lys Tyr Ile Leu
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 Asp Phe Ile Ala Ala Leu Val Ser Ala Phe Asp Ile Gly Glu Glu Lys
 165 170 175
 Thr Arg Val Gly Val Val Gln Tyr Ser Ser Asp Thr Arg Thr Glu Phe
 180 185 190
 Asn Leu Asn Gln Tyr Tyr Gln Arg Asp Glu Leu Leu Ala Ala Ile Lys
 195 200 205
 Lys Ile Pro Tyr Lys Gly Gly Asn Thr Met Thr Gly Asp Ala Ile Asp
 210 215 220
 Tyr Leu Val Lys Asn Thr Phe Thr Glu Ser Ala Gly Ala Arg Val Gly
 225 230 235 240
 Phe Pro Lys Val Ala Ile Ile Ile Thr Asp Gly Lys Ser Gln Asp Glu
 245 250 255
 Val Glu Ile Pro Ala Arg Glu Leu Arg Asn Val Gly Val Glu Val Phe
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 Ser Leu Gly Ile Lys Ala Ala Asp Ala Lys Glu Leu Lys Gln Ile Ala
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 Ser Thr Pro Ser Leu Asn His Val Phe Asn Val Ala Asn Phe Asp Ala
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 Asp Glu Gln Leu Gly Glu Leu Val Ser Gly Glu Glu Val Val Glu Pro
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 Asn Trp Asn Pro Ser Pro Ser Pro Val Thr Gly Tyr Lys Val Ile Leu
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 405 410 415
 Ser Ile Met Glu Lys Thr Gln Pro Met Lys Val Gln Val Glu Cys Ser
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 Arg Gly Val Asp Ile Lys Ala Asp Ile Val Phe Leu Val Asp Gly Ser
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 465 470 475 480
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Lys Asp Ala Val Arg Ser Glu Leu Glu Ala Ile Ala Ser Pro Pro Ala			
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Glu Thr His Val Phe Thr Val Glu Asp Phe Asp Ala Phe Gln Arg Ile			
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Ser Phe Glu Leu Thr Gln Ser Ile Cys Leu Arg Ile Glu Gln Glu Leu			
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Ala Ala Ile Lys Lys Ala Tyr Val Pro Pro Lys Asp Leu Ser Phe			
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Ser Glu Val Thr Ser Tyr Gly Phe Lys Thr Asn Trp Ser Pro Ala Gly			
645	650	655	
Glu Asn Val Phe Ser Tyr His Ile Thr Tyr Lys Glu Ala Ala Gly Asp			
660	665	670	
Asp Glu Val Thr Val Val Glu Pro Ala Ser Ser Thr Ser Val Val Leu			
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Ser Ser Leu Lys Pro Glu Thr Leu Tyr Leu Val Asn Val Thr Ala Glu			
690	695	700	
Tyr Glu Asp Gly Phe Ser Ile Pro Leu Ala Gly Glu Glu Thr Thr Glu			
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Asp Ser Phe Lys Ile Thr Trp Thr Gln Ala Pro Gly Arg Val Leu Arg			
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Cys Arg Ile Ile Tyr Arg Pro Val Ala Gly Gly Glu Ser Arg Glu Val			
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Pro Arg Asp Leu Arg Val Ser Asp Pro Thr Thr Ser Thr Met Lys Leu			
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Ser Trp Ser Gly Ala Pro Gly Lys Val Lys Gln Tyr Leu Val Thr Tyr			
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Thr Pro Val Ala Gly Gly Glu Thr Gln Glu Val Thr Val Arg Gly Asp			
850	855	860	
Thr Thr Asn Thr Val Leu Gln Gly Leu Lys Glu Gly Thr Gln Tyr Ala			
865	870	875	880
Leu Ser Val Thr Ala Leu Tyr Ala Ser Gly Ala Gly Asp Ala Leu Phe			
885	890	895	
Gly Glu Gly Thr Thr Leu Glu Glu Arg Gly Ser Pro Gln Asp Leu Val			
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Thr Lys Asp Ile Thr Asp Thr Ser Ile Gly Ala Tyr Trp Thr Ser Ala			
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Pro Gly Met Val Arg Gly Tyr Arg Val Ser Trp Lys Ser Leu Tyr Asp			
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Asp Val Asp Thr Gly Glu Lys Asn Leu Pro Glu Asp Ala Ile His Thr			
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Met Ile Glu Asn Leu Gln Pro Glu Thr Lys Tyr Arg Ile Ser Val Phe			
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Asn Tyr Arg Val Val Tyr Arg Pro His Gly Arg Gly Lys Gln Met Val			
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2005	2010	2015	

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2565	2570	2575
Tyr Thr Ile Ile Leu Leu Phe Arg Leu Leu Pro Glu Thr Pro Ser Asp		
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Pro Phe Ala Ile Trp Gln Ile Thr Asp Arg Asp Tyr Lys Pro Gln Val		
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Gly Val Ile Ala Asp Pro Ser Ser Lys Thr Leu Ser Phe Phe Asn Lys		
2610	2615	2620
Asp Thr Arg Gly Glu Val Gln Thr Val Thr Phe Asp Thr Glu Glu Val		
2625	2630	2635
2640		
Lys Thr Leu Phe Tyr Gly Ser Phe His Lys Val His Ile Val Val Thr		
2645	2650	2655
Ser Lys Ser Val Lys Ile Tyr Ile Asp Cys Tyr Glu Ile Ile Glu Lys		
2660	2665	2670
Asp Ile Lys Glu Ala Gly Asn Ile Thr Thr Asp Gly Tyr Glu Ile Leu		
2675	2680	2685
Gly Lys Leu Leu Lys Gly Glu Arg Lys Ser Ala Ala Phe Gln Ile Gln		
2690	2695	2700
Ser Phe Asp Ile Val Cys Ser Pro Val Trp Thr Ser Arg Asp Arg Cys		
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2720		
Cys Asp Ile Pro Ser Arg Arg Asp Glu Gly Lys Cys Pro Ala Phe Pro		
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Gly Pro Ala Gly Gly Pro Gly Ala Lys Gly Pro Arg Gly Glu Arg Gly		
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Ile Ser Gly Ala Ile Gly Pro Pro Gly Pro Arg Gly Asp Ile Gly Pro		
2770	2775	2780
Pro Gly Pro Gln Gly Pro Pro Gly Pro Gln Gly Pro Asn Gly Leu Ser		
2785	2790	2795
2800		
Ile Pro Gly Glu Gln Gly Arg Gln Gly Met Lys Gly Asp Ala Gly Glu		
2805	2810	2815
Pro Gly Leu Pro Gly Arg Thr Gly Thr Pro Gly Leu Pro Gly Pro Pro		
2820	2825	2830
Gly Pro Met Gly Pro Pro Gly Asp Arg Gly Phe Thr Gly Lys Asp Ser		
2835	2840	2845
Ala Met Gly Pro Arg Gly Pro Pro Gly Arg Pro Gly Ser Pro Gly Ser		
2850	2855	2860
Pro Gly Val Thr Gly Pro Ser Gly Lys Pro Gly Lys Pro Gly Asp His		
2865	2870	2875
2880		
Gly Arg Pro Gly Pro Ser Gly Leu Lys Gly Glu Lys Gly Asp Arg Gly		
2885	2890	2895
Asp Ile Ala Ser Gln Asn Met Met Arg Ala Val Ala Arg Gln Val Cys		
2900	2905	2910
Glu Gln Leu Ile Ser Gly Gln Met Asn Arg Phe Asn Gln Met Leu Asn		
2915	2920	2925
Gln Ile Pro Asn Asp Tyr Gln Ser Ser Arg Asn Gln Pro Gly Pro Pro		
2930	2935	2940
Gly Pro Pro Gly Pro Pro Gly Ser Ala Gly Ala Arg Gly Glu Pro Gly		
2945	2950	2955
2960		
Pro Gly Gly Arg Pro Gly Phe Pro Gly Thr Pro Gly Met Gln Gly Pro		
2965	2970	2975
Pro Gly Glu Arg Gly Leu Pro Gly Glu Lys Gly Glu Arg Gly Thr Gly		
2980	2985	2990

Ser Ser Gly Pro Arg Gly Leu Pro Gly Pro Pro Gly Pro Gln Gly Glu
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 Ser Arg Thr Gly Pro Pro Gly Ser Thr Gly Ser Arg Gly Pro Pro Gly
 3010 3015 3020
 Pro Pro Gly Arg Pro Gly Asn Ser Gly Ile Gln Gly Pro Pro Gly Pro
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 Gln Ser Tyr Pro Gly Ser Gly
 3060

<210> 258
 <211> 1717
 <212> DNA
 <213> Homo sapiens

<400> 258

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tcatcaccaa	actgtgcacc	agaatgtaac	tgccctgaaa	gctacccaag	tgccatgtac	240
tgtgtatgagc	tgaaattgaa	aagtgtacca	atggtgctc	ctggaatcaa	gtatcttac	300
ccttaggaata	accagattga	ccatattgat	aaaaaggcct	ttgagaatgt	aactgatctg	360
cagtggtctca	ttcttagatca	caaccttcta	aaaaactcca	agataaaaagg	gagagtttc	420
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ttcaatcaga	tagccagact	gccttctgg	ctccctgtct	ctttctaaac	tctctactta	720
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<210> 259
 <211> 338
 <212> PRT
 <213> Homo sapiens

<400> 259

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					20				25				30		
Ser	Ser	Pro	Asn	Cys	Ala	Pro	Glu	Cys	Asn	Cys	Pro	Glu	Ser	Tyr	Pro
					35				40				45		
Ser	Ala	Met	Tyr	Cys	Asp	Glu	Leu	Lys	Leu	Lys	Ser	Val	Pro	Met	Val
					50				55				60		

Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His
 65 70 75 80
 Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile
 85 90 95
 Leu Asp His Asn Leu Leu Glu Asn Ser Lys Ile Lys Gly Arg Val Phe
 100 105 110
 Ser Lys Leu Lys Gln Leu Lys Lys Leu His Ile Asn His Asn Asn Leu
 115 120 125
 Thr Glu Ser Val Gly Pro Leu Pro Lys Ser Leu Glu Asp Leu Gln Leu
 130 135 140
 Thr His Asn Lys Ile Thr Lys Leu Gly Ser Phe Glu Gly Leu Val Asn
 145 150 155 160
 Leu Thr Phe Ile His Leu Gln His Asn Arg Leu Lys Glu Asp Ala Val
 165 170 175
 Ser Ala Ala Phe Lys Gly Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser
 180 185 190
 Phe Asn Gln Ile Ala Arg Leu Pro Ser Gly Leu Pro Val Ser Leu Leu
 195 200 205
 Thr Leu Tyr Leu Asp Asn Asn Lys Ile Ser Asn Ile Pro Asp Glu Tyr
 210 215 220
 Phe Lys Arg Phe Asn Ala Leu Gln Tyr Leu Arg Leu Ser His Asn Glu
 225 230 235 240
 Leu Ala Asp Ser Gly Ile Pro Gly Asn Ser Phe Asn Val Ser Ser Leu
 245 250 255
 Val Glu Leu Asp Leu Ser Tyr Asn Lys Leu Lys Asn Ile Pro Thr Val
 260 265 270
 Asn Glu Asn Leu Glu Asn Tyr Tyr Leu Glu Val Asn Gln Leu Glu Lys
 275 280 285
 Phe Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser
 290 295 300
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 305 310 315 320
 Leu Pro Pro Asp Met Tyr Glu Cys Leu Arg Val Ala Asn Glu Val Thr
 325 330 335
 Leu Asn

<210> 260
 <211> 6728
 <212> DNA
 <213> Homo sapiens

<400> 260

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gcgtctgcga caacggcaag gtgttgtgcg atgacgtgat ctgtgacgag accaagaact	360
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cctgg	ccgt	ccat	ccat	ccat	ccat	4440
atgt	gggg	gtgg	gtgg	ccat	ccat	4500
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ccca	actcc	ccat	ccat	ccat	ccat	4620
agaca	atttc	ccat	ccat	ccat	ccat	4680
agtttt	tatc	ccat	ccat	ccat	ccat	4740

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<210> 261
 <211> 1464
 <212> PRT
 <213> Homo sapiens

<400> 261
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 20 25 30
 Glu Asp Ile Pro Pro Ile Thr Cys Val Gln Asn Gly Leu Arg Tyr His
 35 40 45
 Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Arg Ile Cys Val Cys Asp
 50 55 60
 Asn Gly Lys Val Leu Cys Asp Asp Val Ile Cys Asp Glu Thr Lys Asn
 65 70 75 80
 Cys Pro Gly Ala Glu Val Pro Glu Gly Glu Cys Cys Pro Val Cys Pro
 85 90 95
 Asp Gly Ser Glu Ser Pro Thr Asp Gln Glu Thr Thr Gly Val Glu Gly
 100 105 110
 Pro Lys Gly Asp Thr Gly Pro Arg Gly Pro Arg Gly Pro Ala Gly Pro
 115 120 125
 Pro Gly Arg Asp Gly Ile Pro Gly Gln Pro Gly Leu Pro Gly Pro Pro
 130 135 140

Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala
 145 150 155 160
 Pro Gln Leu Ser Tyr Gly Tyr Asp Glu Lys Ser Thr Gly Gly Ile Ser
 165 170 175
 Val Pro Gly Pro Met Gly Pro Ser Gly Pro Arg Gly Leu Pro Gly Pro
 180 185 190
 Pro Gly Ala Pro Gly Pro Gln Gly Phe Gln Gly Pro Pro Gly Glu Pro
 195 200 205
 Gly Glu Pro Gly Ala Ser Gly Pro Met Gly Pro Arg Gly Pro Pro Gly
 210 215 220
 Pro Pro Gly Lys Asn Gly Asp Asp Gly Glu Ala Gly Lys Pro Gly Arg
 225 230 235 240
 Pro Gly Glu Arg Gly Pro Pro Gly Pro Gln Gly Ala Arg Gly Leu Pro
 245 250 255
 Gly Thr Ala Gly Leu Pro Gly Met Lys Gly His Arg Gly Phe Ser Gly
 260 265 270
 Leu Asp Gly Ala Lys Gly Asp Ala Gly Pro Ala Gly Pro Lys Gly Glu
 275 280 285
 Pro Gly Ser Pro Gly Glu Asn Gly Ala Pro Gly Gln Met Gly Pro Arg
 290 295 300
 Gly Leu Pro Gly Glu Arg Gly Arg Pro Gly Ala Pro Gly Pro Ala Gly
 305 310 315 320
 Ala Arg Gly Asn Asp Gly Ala Thr Gly Ala Ala Gly Pro Pro Gly Pro
 325 330 335
 Thr Gly Pro Ala Gly Pro Pro Gly Phe Pro Gly Ala Val Gly Ala Lys
 340 345 350
 Gly Glu Ala Gly Pro Gln Gly Pro Arg Gly Ser Glu Gly Pro Gln Gly
 355 360 365
 Val Arg Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Ala Ala Gly Pro
 370 375 380
 Ala Gly Asn Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys Gly Ala Asn
 385 390 395 400
 Gly Ala Pro Gly Ile Ala Gly Ala Pro Gly Phe Pro Gly Ala Arg Gly
 405 410 415
 Pro Ser Gly Pro Gln Gly Pro Gly Gly Pro Pro Gly Pro Lys Gly Asn
 420 425 430
 Ser Gly Glu Pro Gly Ala Pro Gly Ser Lys Gly Asp Thr Gly Ala Lys
 435 440 445
 Gly Glu Pro Gly Pro Val Gly Val Gln Gly Pro Pro Gly Pro Ala Gly
 450 455 460
 Glu Glu Gly Lys Arg Gly Ala Arg Gly Glu Pro Gly Pro Thr Gly Leu
 465 470 475 480
 Pro Gly Pro Pro Gly Glu Arg Gly Gly Pro Gly Ser Arg Gly Phe Pro
 485 490 495
 Gly Ala Asp Gly Val Ala Gly Pro Lys Gly Pro Ala Gly Glu Arg Gly
 500 505 510
 Ser Pro Gly Pro Ala Gly Pro Lys Gly Ser Pro Gly Glu Ala Gly Arg
 515 520 525
 Pro Gly Glu Ala Gly Leu Pro Gly Ala Lys Gly Leu Thr Gly Ser Pro
 530 535 540
 Gly Ser Pro Gly Pro Asp Gly Lys Thr Gly Pro Pro Gly Pro Ala Gly
 545 550 555 560
 Gln Asp Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Ala Arg Gly Gln
 565 570 575
 Ala Gly Val Met Gly Phe Pro Gly Pro Lys Gly Ala Ala Gly Glu Pro
 580 585 590
 Gly Lys Ala Gly Glu Arg Gly Val Pro Gly Pro Pro Gly Ala Val Gly
 595 600 605
 Pro Ala Gly Lys Asp Gly Glu Ala Gly Ala Gln Gly Pro Pro Gly Pro
 610 615 620
 Ala Gly Pro Ala Gly Glu Arg Gly Glu Gln Gly Pro Ala Gly Ser Pro

625	630	635	640
Gly Phe Gln Gly Leu Pro Gly Pro Ala Gly Pro Pro Gly Glu Ala Gly			
645	650	655	
Lys Pro Gly Glu Gln Gly Val Pro Gly Asp Leu Gly Ala Pro Gly Pro			
660	665	670	
Ser Gly Ala Arg Gly Glu Arg Gly Phe Pro Gly Glu Arg Gly Val Gln			
675	680	685	
Gly Pro Pro Gly Pro Ala Gly Pro Arg Gly Ala Asn Gly Ala Pro Gly			
690	695	700	
Asn Asp Gly Ala Lys Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly Ser			
705	710	715	720
Gln Gly Ala Pro Gly Leu Gln Gly Met Pro Gly Glu Arg Gly Ala Ala			
725	730	735	
Gly Leu Pro Gly Pro Lys Gly Asp Arg Gly Asp Ala Gly Pro Lys Gly			
740	745	750	
Ala Asp Gly Ser Pro Gly Lys Asp Gly Val Arg Gly Leu Thr Gly Pro			
755	760	765	
Ile Gly Pro Pro Gly Pro Ala Gly Ala Pro Gly Asp Lys Gly Glu Ser			
770	775	780	
Gly Pro Ser Gly Pro Ala Gly Pro Thr Gly Ala Arg Gly Ala Pro Gly			
785	790	795	800
Asp Arg Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Phe Ala Gly Pro			
805	810	815	
Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys Gly Glu Pro Gly Asp Ala			
820	825	830	
Gly Ala Lys Gly Asp Ala Gly Pro Pro Gly Pro Ala Gly Pro Ala Gly			
835	840	845	
Pro Pro Gly Pro Ile Gly Asn Val Gly Ala Pro Gly Ala Lys Gly Ala			
850	855	860	
Arg Gly Ser Ala Gly Pro Pro Gly Ala Thr Gly Phe Pro Gly Ala Ala			
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885	890	895	
Pro Pro Gly Pro Ala Gly Lys Glu Gly Lys Gly Pro Arg Gly Glu			
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Thr Gly Pro Ala Gly Arg Pro Gly Glu Val Gly Pro Pro Gly Pro Pro			
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Gly Pro Ala Gly Glu Lys Gly Ser Pro Gly Ala Asp Gly Pro Ala Gly			
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945	950	955	960
Val Gly Leu Pro Gly Gln Arg Gly Glu Arg Gly Phe Pro Gly Leu Pro			
965	970	975	
Gly Pro Ser Gly Glu Pro Gly Lys Gln Gly Pro Ser Gly Ala Ser Gly			
980	985	990	
Glu Arg Gly Pro Pro Gly Pro Met Gly Pro Pro Gly Leu Ala Gly Pro			
995	1000	1005	
Pro Gly Glu Ser Gly Arg Glu Gly Ala Pro Ala Ala Glu Gly Ser Pro			
1010	1015	1020	
Gly Arg Asp Gly Ser Pro Gly Ala Lys Gly Asp Arg Gly Glu Thr Gly			
1025	1030	1035	1040
Pro Ala Gly Pro Pro Gly Ala Pro Gly Ala Pro Gly Ala Pro Gly Pro			
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Val Gly Pro Ala Gly Lys Ser Gly Asp Arg Gly Glu Thr Gly Pro Ala			
1060	1065	1070	
Gly Pro Ala Gly Pro Val Gly Pro Val Gly Ala Arg Gly Pro Ala Gly			
1075	1080	1085	
Pro Gln Gly Pro Arg Gly Asp Lys Gly Glu Thr Gly Glu Gln Gly Asp			
1090	1095	1100	
Arg Gly Ile Lys Gly His Arg Gly Phe Ser Gly Leu Gln Gly Pro Pro			
1105	1110	1115	1120

Gly Pro Pro Gly Ser Pro Gly Glu Gln Gly Pro Ser Gly Ala Ser Gly
 1125 1130 1135
 Pro Ala Gly Pro Arg Gly Pro Pro Gly Ser Ala Gly Ala Pro Gly Lys
 1140 1145 1150
 Asp Gly Leu Asn Gly Leu Pro Gly Pro Ile Gly Pro Pro Gly Pro Arg
 1155 1160 1165
 Gly Arg Thr Gly Asp Ala Gly Pro Val Gly Pro Pro Gly Pro Pro Gly
 1170 1175 1180
 Pro Pro Gly Pro Pro Gly Pro Pro Ser Ala Gly Phe Asp Phe Ser Phe
 1185 1190 1195 1200
 Leu Pro Gln Pro Pro Gln Glu Lys Ala His Asp Gly Gly Arg Tyr Tyr
 1205 1210 1215
 Arg Ala Asp Asp Ala Asn Val Val Arg Asp Arg Asp Leu Glu Val Asp
 1220 1225 1230
 Thr Thr Leu Lys Ser Leu Ser Gln Gln Ile Glu Asn Ile Arg Ser Pro
 1235 1240 1245
 Glu Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys Arg Asp Leu Lys Met
 1250 1255 1260
 Cys His Ser Asp Trp Lys Ser Gly Glu Tyr Trp Ile Asp Pro Asn Gln
 1265 1270 1275 1280
 Gly Cys Asn Leu Asp Ala Ile Lys Val Phe Cys Asn Met Glu Thr Gly
 1285 1290 1295
 Glu Thr Cys Val Tyr Pro Thr Gln Pro Ser Val Ala Gln Lys Asn Trp
 1300 1305 1310
 Tyr Ile Ser Lys Asn Pro Lys Asp Lys Arg His Val Trp Phe Gly Glu
 1315 1320 1325
 Ser Met Thr Asp Gly Phe Gln Phe Glu Tyr Gly Gly Gln Gly Ser Asp
 1330 1335 1340
 Pro Ala Asp Val Ala Ile Gln Leu Thr Phe Leu Arg Leu Met Ser Thr
 1345 1350 1355 1360
 Glu Ala Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Val Ala Tyr
 1365 1370 1375
 Met Asp Gln Gln Thr Gly Asn Leu Lys Lys Ala Leu Leu Leu Lys Gly
 1380 1385 1390
 Ser Asn Glu Ile Glu Ile Arg Ala Glu Gly Asn Ser Arg Phe Thr Tyr
 1395 1400 1405
 Ser Val Thr Val Asp Gly Cys Thr Ser His Thr Gly Ala Trp Gly Lys
 1410 1415 1420
 Thr Val Ile Glu Tyr Lys Thr Thr Lys Ser Ser Arg Leu Pro Ile Ile
 1425 1430 1435 1440
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 1445 1450 1455
 Asp Val Gly Pro Val Cys Phe Leu
 1460

<210> 262

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 262

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gaagaagagg	gttggaaagcca	ttaggggaca	gatcttgagc	aagctcaggc	tcaccagccc	420
ccctgagcca	acggtgatga	cccacgtccc	ctatcaggc	ctggcccttt	acaacagcac	480
ccgggagctg	ctggaggaga	tgcatgggaa	gagggaggaa	ggctgcaccc	aggaaaacac	540
cgagtcggaa	tactatgcca	aagaaatcca	taaattcgac	atgatccagg	ggctggcgga	600

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agatatc	aaa	acattc	acgagg	gaaatcaaa	ttcaaaggcg	1020
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tcatcta	atc	tc	catgt	ccgg	accacaaccc	1140
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tgtgc	ccc	tc	tacatt	acttccg	gatctgggc	1260
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aaccac	ac	gca	actgt	cact	gtgcagacac	1380
ttgctgc	cc	cc	gactgt	ctgt	ctgcctcgcc	1440
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gctctagg	at	ct	tttgc	ttt	ggat	1980
acgaagaca	ag	cc	tgt	ttt	tttgc	2040
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ggtcatgc	tt	cc	catca	ttt	tttgc	2160
gaaagg	aa	at	att	ttt	tttgc	2220
tcgatcat	tt	cc	actgt	ttt	tttgc	2280
tggattgt	tt	cc	tttgc	ttt	tttgc	2340
accctgt	catt	tttgc	tttgc	tttgc	tttgc	2400
agctgcacat	gt	cc	tttgc	tttgc	tttgc	2460
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<210> 263

<211> 412

<212> PRT

<213> Homo sapiens

<400> 263

Met	Lys	Met	His	Leu	Gln	Arg	Ala	Leu	Val	Val	Leu	Ala	Leu	Leu	Asn
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Phe	Ala	Thr	Val	Ser	Leu	Ser	Leu	Ser	Thr	Cys	Thr	Thr	Leu	Asp	Phe
								20		25		30			
Gly	His	Ile	Lys	Lys	Lys	Arg	Val	Glu	Ala	Ile	Arg	Gly	Gln	Ile	Leu
							35		40		45				
Ser	Lys	Leu	Arg	Leu	Thr	Ser	Pro	Pro	Glu	Pro	Thr	Val	Met	Thr	His
						50		55		60					
Val	Pro	Tyr	Gln	Val	Leu	Ala	Leu	Tyr	Asn	Ser	Thr	Arg	Glu	Leu	Leu
						65		70		75		80			
Glu	Glu	Met	His	Gly	Glu	Arg	Glu	Glu	Gly	Cys	Thr	Gln	Glu	Asn	Thr
						85		90		95					
Glu	Ser	Glu	Tyr	Tyr	Ala	Lys	Glu	Ile	His	Lys	Phe	Asp	Met	Ile	Gln
						100		105		110					
Gly	Leu	Ala	Glu	His	Asn	Glu	Leu	Ala	Val	Cys	Pro	Lys	Gly	Ile	Thr
						115		120		125					
Ser	Lys	Val	Phe	Arg	Phe	Asn	Val	Ser	Ser	Val	Glu	Lys	Asn	Arg	Thr
						130		135		140					
Asn	Leu	Phe	Arg	Ala	Glu	Phe	Arg	Val	Leu	Arg	Val	Pro	Asn	Pro	Ser
						145		150		155		160			
Ser	Lys	Arg	Asn	Glu	Gln	Arg	Ile	Glu	Leu	Phe	Gln	Ile	Leu	Arg	Pro

/

Asp	Glu	His	Ile	Ala	Lys	Gln	Arg	Tyr	Ile	Gly	Gly	Lys	Asn	Leu	Pro
165								170					175		
180								185					190		
Thr	Arg	Gly	Thr	Ala	Glu	Trp	Leu	Ser	Phe	Asp	Val	Thr	Asp	Thr	Val
195							200					205			
Arg	Glu	Trp	Leu	Leu	Arg	Arg	Glu	Ser	Asn	Leu	Gly	Leu	Glu	Ile	Ser
210							215				220				
Ile	His	Cys	Pro	Cys	His	Thr	Phe	Gln	Pro	Asn	Gly	Asp	Ile	Leu	Glu
225							230				235			240	
Asn	Ile	His	Glu	Val	Met	Glu	Ile	Lys	Phe	Lys	Gly	Val	Asp	Asn	Glu
245							250						255		
Asp	Asp	His	Gly	Arg	Gly	Asp	Leu	Gly	Arg	Leu	Lys	Lys	Gln	Lys	Asp
260							265						270		
His	His	Asn	Pro	His	Leu	Ile	Leu	Met	Met	Ile	Pro	Pro	His	Arg	Leu
275							280						285		
Asp	Asn	Pro	Gly	Gln	Gly	Gly	Gln	Arg	Lys	Lys	Arg	Ala	Leu	Asp	Thr
290							295						300		
Asn	Tyr	Cys	Phe	Arg	Asn	Leu	Glu	Glu	Asn	Cys	Cys	Val	Arg	Pro	Leu
305							310				315			320	
Tyr	Ile	Asp	Phe	Arg	Gln	Asp	Leu	Gly	Trp	Lys	Trp	Val	His	Glu	Pro
325							330						335		
Lys	Gly	Tyr	Tyr	Ala	Asn	Phe	Cys	Ser	Gly	Pro	Cys	Pro	Tyr	Leu	Arg
340							345						350		
Ser	Ala	Asp	Thr	Thr	His	Ser	Thr	Val	Leu	Gly	Leu	Tyr	Asn	Thr	Leu
355							360						365		
Asn	Pro	Glú	Ala	Ser	Ala	Ser	Pro	Cys	Cys	Val	Pro	Gln	Asp	Leu	Glu
370							375						380		
Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Val	Gly	Arg	Thr	Pro	Lys	Val	Glu	Gln
385							390						395		400
Leu	Ser	Asn	Met	Val	Val	Lys	Ser	Cys	Lys	Cys	Ser				
							405						410		

<210> 264

<211> 5086

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(5086)

<223> n = A,T,C or G

<400> 264

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gcatgtctaa	gtgctagaca	tgctcagctt	tgtggatacg	cggaaccttgc	tgctgcttgc	180
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tgaagatgg	cccacaggcc	ctccctggtcc	acctggtcct	cctggccccc	ctggctcgg	360
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<210> 265
<211> 1366
<212> PRT
<213> Homo sapiens

<400> 265

Met	Leu	Ser	Phe	Val	Asp	Thr	Arg	Thr	Leu	Leu	Leu	Leu	Ala	Val	Thr
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						20			25					30	
Gly	Pro	Ala	Gly	Asp	Arg	Gly	Pro	Arg	Gly	Glu	Arg	Gly	Pro	Pro	Gly
				35				40				45			
Pro	Pro	Gly	Arg	Asp	Gly	Glu	Asp	Gly	Pro	Thr	Gly	Pro	Pro	Gly	Pro
					50		55			60					
Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Leu	Gly	Gly	Asn	Phe	Ala	Ala	Gln
					65		70			75				80	
Tyr	Asp	Gly	Lys	Gly	Val	Gly	Leu	Gly	Pro	Gly	Pro	Met	Gly	Leu	Met
					85			90			95				
Gly	Pro	Arg	Gly	Pro	Pro	Gly	Ala	Ala	Gly	Ala	Pro	Gly	Pro	Gln	Gly
				100				105			110				
Phe	Gln	Gly	Pro	Ala	Gly	Glu	Pro	Gly	Glu	Pro	Gly	Gln	Thr	Gly	Pro
				115				120			125				
Ala	Gly	Ala	Arg	Gly	Pro	Ala	Gly	Pro	Pro	Gly	Lys	Ala	Gly	Glu	Asp
				130				135			140				
Gly	His	Pro	Gly	Lys	Pro	Gly	Arg	Pro	Gly	Glu	Arg	Gly	Val	Val	Gly
				145				150			155			160	
Pro	Gln	Gly	Ala	Arg	Gly	Phe	Pro	Gly	Thr	Pro	Gly	Leu	Pro	Gly	Phe
					165			170			175				
Lys	Gly	Ile	Arg	Gly	His	Asn	Gly	Leu	Asp	Gly	Leu	Lys	Gly	Gln	Pro
				180				185			190				
Gly	Ala	Pro	Gly	Val	Lys	Gly	Glu	Pro	Gly	Ala	Pro	Gly	Glu	Asn	Gly
				195				200			205				
Thr	Pro	Gly	Gln	Thr	Gly	Ala	Arg	Gly	Leu	Pro	Gly	Glu	Arg	Gly	Arg
				210				215			220				
Val	Gly	Ala	Pro	Gly	Pro	Ala	Gly	Ala	Arg	Gly	Ser	Asp	Gly	Ser	Val
				225				230			235			240	
Gly	Pro	Val	Gly	Pro	Ala	Gly	Pro	Ile	Gly	Ser	Ala	Gly	Pro	Pro	Gly
					245			250			255				
Phe	Pro	Gly	Ala	Pro	Gly	Pro	Lys	Gly	Ile	Gly	Ala	Val	Gly	Asn	
					260			265			270				
Ala	Gly	Pro	Ala	Gly	Pro	Ala	Gly	Pro	Arg	Gly	Glu	Val	Gly	Leu	Pro
				275				280			285				
Gly	Leu	Ser	Gly	Pro	Val	Gly	Pro	Pro	Gly	Asn	Pro	Gly	Ala	Asn	Gly
				290				295			300				
Leu	Thr	Gly	Ala	Lys	Gly	Ala	Ala	Gly	Leu	Pro	Gly	Val	Ala	Gly	Ala
				305				310			315			320	
Pro	Gly	Leu	Pro	Gly	Pro	Arg	Gly	Ile	Pro	Gly	Pro	Val	Gly	Ala	Ala
					325			330			335				
Gly	Ala	Thr	Gly	Ala	Arg	Gly	Leu	Val	Gly	Glu	Pro	Gly	Pro	Ala	Gly
					340			345			350				
Ser	Lys	Gly	Glu	Ser	Gly	Asn	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Pro
				355				360			365				

Gln Gly Pro Pro Gly Pro Ser Gly Glu Glu Gly Lys Arg Gly Pro Asn
 370 375 380
 Gly Glu Ala Gly Ser Ala Gly Pro Pro Gly Pro Pro Gly Leu Arg Gly
 385 390 395 400
 Ser Pro Gly Ser Arg Gly Leu Pro Gly Ala Asp Gly Arg Ala Gly Val
 405 410 415
 Met Gly Pro Pro Gly Ser Arg Gly Ala Ser Gly Pro Ala Gly Val Arg
 420 425 430
 Gly Pro Asn Gly Asp Ala Gly Arg Pro Gly Glu Pro Gly Leu Met Gly
 435 440 445
 Pro Arg Gly Leu Pro Gly Ser Pro Gly Asn Ile Gly Pro Ala Gly Lys
 450 455 460
 Glu Gly Pro Val Gly Leu Pro Gly Ile Asp Gly Arg Pro Gly Pro Ile
 465 470 475 480
 Gly Pro Ala Gly Ala Arg Gly Glu Pro Gly Asn Ile Gly Phe Pro Gly
 485 490 495
 Pro Lys Gly Pro Thr Gly Asp Pro Gly Lys Asn Gly Asp Lys Gly His
 500 505 510
 Ala Gly Leu Ala Gly Ala Arg Gly Ala Pro Gly Pro Asp Gly Asn Asn
 515 520 525
 Gly Ala Gln Gly Pro Pro Gly Pro Gln Gly Val Gln Gly Lys Gly
 530 535 540
 Glu Gln Gly Pro Ala Gly Pro Pro Gly Phe Gln Gly Leu Pro Gly Pro
 545 550 555 560
 Ser Gly Pro Ala Gly Glu Val Gly Lys Pro Gly Glu Arg Gly Leu His
 565 570 575
 Gly Glu Phe Gly Leu Pro Gly Pro Ala Gly Pro Arg Gly Glu Arg Gly
 580 585 590
 Pro Pro Gly Glu Ser Gly Ala Ala Gly Pro Thr Gly Pro Ile Gly Ser
 595 600 605
 Arg Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly Asn Lys Gly Glu Pro
 610 615 620
 Gly Val Val Gly Ala Val Gly Thr Ala Gly Pro Ser Gly Pro Ser Gly
 625 630 635 640
 Leu Pro Gly Glu Arg Gly Ala Ala Gly Ile Pro Gly Gly Lys Gly Glu
 645 650 655
 Lys Gly Glu Pro Gly Leu Arg Gly Glu Ile Gly Asn Pro Gly Arg Asp
 660 665 670
 Gly Ala Arg Gly Ala His Gly Ala Val Gly Ala Pro Gly Pro Ala Gly
 675 680 685
 Ala Thr Gly Asp Arg Gly Glu Ala Gly Ala Ala Gly Pro Ala Gly Pro
 690 695 700
 Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Val Gly Pro Ala
 705 710 715 720
 Gly Pro Asn Gly Phe Ala Gly Pro Ala Gly Ala Ala Gly Gln Pro Gly
 725 730 735
 Ala Lys Gly Glu Arg Gly Ala Lys Gly Pro Lys Gly Glu Asn Gly Val
 740 745 750
 Val Gly Pro Thr Gly Pro Val Gly Ala Ala Gly Pro Ala Gly Pro Asn
 755 760 765
 Gly Pro Pro Gly Pro Ala Gly Ser Arg Gly Asp Gly Gly Pro Pro Gly
 770 775 780
 Met Thr Gly Phe Pro Gly Ala Ala Gly Arg Thr Gly Pro Pro Gly Pro
 785 790 795 800
 Ser Gly Ile Ser Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Lys Glu
 805 810 815
 Gly Leu Arg Gly Pro Arg Gly Asp Gln Gly Pro Val Gly Arg Thr Gly
 820 825 830
 Glu Val Gly Ala Val Gly Pro Pro Gly Phe Ala Gly Glu Lys Gly Pro
 835 840 845
 Ser Gly Glu Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly Pro Gln

850	855	860
Gly Leu Leu Gly Ala Pro Gly Ile Leu Gly Leu Pro Gly Ser Arg Gly		
865	870	875
Glu Arg Gly Leu Pro Gly Val Ala Gly Ala Val Gly Glu Pro Gly Pro		880
885	890	895
Leu Gly Ile Ala Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Ala Val		
900	905	910
Gly Ser Pro Gly Val Asn Gly Ala Pro Gly Glu Ala Gly Arg Asp Gly		
915	920	925
Asn Pro Gly Asn Asp Gly Pro Pro Gly Arg Asp Gly Gln Pro Gly His		
930	935	940
Lys Gly Glu Arg Gly Tyr Pro Gly Asn Ile Gly Pro Val Gly Ala Ala		
945	950	955
Gly Ala Pro Gly Pro His Gly Pro Val Gly Pro Ala Gly Lys His Gly		960
965	970	975
Asn Arg Gly Glu Thr Gly Pro Ser Gly Pro Val Gly Pro Ala Gly Ala		
980	985	990
Val Gly Pro Arg Gly Pro Ser Gly Pro Gln Gly Ile Arg Gly Asp Lys		
995	1000	1005
Gly Glu Pro Gly Glu Lys Gly Pro Arg Gly Leu Pro Gly Leu Lys Gly		
1010	1015	1020
His Asn Gly Leu Gln Gly Leu Pro Gly Ile Ala Gly His His Gly Asp		
1025	1030	1035
Gln Gly Ala Pro Gly Ser Val Gly Pro Ala Gly Pro Arg Gly Pro Ala		
1045	1050	1055
Gly Pro Ser Gly Pro Ala Gly Lys Asp Gly Arg Thr Gly His Pro Gly		
1060	1065	1070
Thr Val Gly Pro Ala Gly Ile Arg Gly Pro Gln Gly His Gln Gly Pro		
1075	1080	1085
Ala Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Val Ser		
1090	1095	1100
Gly Gly Gly Tyr Asp Phe Gly Tyr Asp Gly Asp Phe Tyr Arg Ala Asp		
1105	1110	1115
Gln Pro Arg Ser Ala Pro Ser Leu Arg Pro Lys Asp Tyr Glu Val Asp		
1125	1130	1135
Ala Thr Leu Lys Ser Leu Asn Asn Gln Ile Glu Thr Leu Leu Thr Pro		
1140	1145	1150
Glu Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys Arg Asp Leu Arg Leu		
1155	1160	1165
Ser His Pro Glu Trp Ser Ser Gly Tyr Tyr Trp Ile Asp Pro Asn Gln		
1170	1175	1180
Gly Cys Thr Met Asp Ala Ile Lys Val Tyr Cys Asp Phe Ser Thr Gly		
1185	1190	1195
Glu Thr Cys Ile Arg Ala Gln Pro Glu Asn Ile Pro Ala Lys Asn Trp		
1205	1210	1215
Tyr Arg Ser Ser Lys Asp Lys Lys His Val Trp Leu Gly Glu Thr Ile		
1220	1225	1230
Asn Ala Gly Ser Gln Phe Glu Tyr Asn Val Glu Gly Val Thr Ser Lys		
1235	1240	1245
Glu Met Ala Thr Gln Leu Ala Phe Met Arg Leu Leu Ala Asn Tyr Ala		
1250	1255	1260
Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Ile Ala Tyr Met Asp		
1265	1270	1275
Glu Glu Thr Gly Asn Leu Lys Lys Ala Val Ile Leu Gln Gly Ser Asn		
1285	1290	1295
Asp Val Glu Leu Val Ala Glu Gly Asn Ser Arg Phe Thr Tyr Thr Val		
1300	1305	1310
Leu Val Asp Gly Cys Ser Lys Lys Thr Asn Glu Trp Gly Lys Thr Ile		
1315	1320	1325
Ile Glu Tyr Lys Thr Asn Lys Pro Ser Arg Leu Pro Phe Leu Asp Ile		
1330	1335	1340

Ala Pro Leu Asp Ile Gly Gly Ala Asp His Glu Phe Phe Val Asp Ile
 1345 1350 1355 1360
 Gly Pro Val Cys Phe Lys
 1365

<210> 266
 <211> 2028
 <212> DNA
 <213> Homo sapiens

<400> 266

atggcatatg caaaagccct gaggctgcag tggagagagc cattgaaagg gaaggccaat	60
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gcagcaactc actggagccc ctcttgc(ccc ccgcaacagg ttttgggga cctggaccag	180
gtgaggatga cctcggaggg ctccgactgc cgttgcaagt gcatcatgcg gcccctgagc	240
aaggacgcgt gtagccgagt ggcgactggg cgggcacgcg tggaggactt ctacacggtg	300
gagactgtga gctcggcac tgactgccc tgctcctgtc cccgacactcc ctccctctc	360
aaccctgtg agaacgagtg gaagatggag aaactcaaaa agcaggccgc cgagctcctc	420
aagctgcgt ccatgttgg tctcttggag ggcacccgt acagcatgga cttgtatgaag	480
gtgacacgcct acgtccacaa ggtggcctcc cagatgaaca cactggaaga gagcatcaag	540
gccaaacctga gccgggagaa tgagggtggta aaggacagcg tgcgccacct cagtgagcag	600
ttgaggcact atgagaatca ctctgcccatt atgctggca tcaagaagga gctgtccgc	660
ctggccctcc agctgctgca gaaggatggc gcccggcccc ctggccacccc tgccacgggc	720
actgttagca aggcccaggaa cacagctaga ggaaaaaggca aggacatcag caagtatggc	780
agtgtgcaga aaagcttgc agacagaggc ctcccaaaaac ctcccaagga gaagctgttt	840
cagggtggaga agctgagaaa ggagagcgcc aaggcagtt tcctccagcc cacagccaag	900
ccccggcccc tggcccccgcga gcaggctgtg atccggggct tcacctacta caaggcaggc	960
aaggcaggagg tgaccgaggc ggtggcagac aacaccctcc agggcacttc ctggctggag	1020
caactgccc ccaagggttga gggcagggtcc aactccgcg agcccaactc cgcagagcag	1080
gatgaggctg agcccgaggc etccgagcga gtggacotttgc ttcttggcac ccccacttca	1140
atccctgcca ccaccaccc cgcaccacc acccccaaccc ccaccaccag tctcctgccc	1200
accgagccac ctccagggtcc agaagtctcc agccaaggca gagaggcggag ctgtgaggc	1260
accctccggg ctgtggaccc ccctgtgagg caccacagct atgggcccga cgaggagcc	1320
tggatgaagg accctgcaggc tcgagacgac aggtatctatg tcaccaacta ctactatgg	1380
aacagcctgg tggagttccg caacctggaa aacttcaagc aagccgcgt gagaacatg	1440
tacaagctac cctacaactg gatggcaca ggccacgtgg tgtaccaggc cgcccttac	1500
tacaaccgcg ccttacccaa gaacatcatc aagtacgacc tacggcagcg cttcgtggcc	1560
tcctggcgcc tgcgtcccgat cgtgttat gaggacacca cacttggaa gtggcgccga	1620
cactcggaca ttgacttgc cgtggacgag agccgcgtt ggtcatcta ccccgccgt	1680
gacgaccgcg atgaggccca gcccggatgt atcgtcttgc gtcgtttggaa cccggcgat	1740
ctctccgtgc accggggagac cacgtggaa acacggcgtc ggccggaaactc ctacggAAC	1800
tgcttcctgg tggcgccat cctgtatgcc gtggacacgt acaaccagca ggaaggccag	1860
gtcgctctacg ctttcgacac gcacacgggc accgacggcac gccccccagct gccgttctc	1920
aacgagcagc cttacaccac ccagatcgac tacaacccca aggagcgggt gctgtacgcc	1980
tggacaatg gccaccagct cacttacacc ctccacttgc tggcttga	2028

<210> 267
 <211> 675
 <212> PRT
 <213> Homo sapiens

<400> 267

Met Ala Tyr Ala Lys Ala Leu Arg Leu Gln Trp Arg Glu Pro Leu Lys	
1 5 10 15	
Gly Lys Gly Asn Lys Glu Arg Phe Lys Gly Glu Tyr Gln Leu Thr Trp	
20 25 30	
Ala Leu Lys Ala Thr His Cys Leu Ala Ala Thr His Trp Ser Pro Ser	
35 40 45	
Cys Pro Pro Gln Gln Val Phe Gly Asp Leu Asp Gln Val Arg Met Thr	
50 55 60	
Ser Glu Gly Ser Asp Cys Arg Cys Lys Cys Ile Met Arg Pro Leu Ser	

65	70	75	80
Lys Asp Ala Cys Ser Arg Val Arg Ser Gly Arg Ala Arg Val Glu Asp			
85	90	95	
Phe Tyr Thr Val Glu Thr Val Ser Ser Gly Thr Asp Cys Arg Cys Ser			
100	105	110	
Cys Thr Ala Pro Pro Ser Ser Leu Asn Pro Cys Glu Asn Glu Trp Lys			
115	120	125	
Met Glu Lys Leu Lys Lys Gln Ala Pro Glu Leu Leu Lys Leu Gln Ser			
130	135	140	
Met Val Asp Leu Leu Glu Gly Thr Leu Tyr Ser Met Asp Leu Met Lys			
145	150	155	160
Val His Ala Tyr Val His Lys Val Ala Ser Gln Met Asn Thr Leu Glu			
165	170	175	
Glu Ser Ile Lys Ala Asn Leu Ser Arg Glu Asn Glu Val Val Lys Asp			
180	185	190	
Ser Val Arg His Leu Ser Glu Gln Leu Arg His Tyr Glu Asn His Ser			
195	200	205	
Ala Ile Met Leu Gly Ile Lys Lys Glu Leu Ser Arg Leu Gly Leu Gln			
210	215	220	
Leu Leu Gln Lys Asp Ala Ala Ala Pro Ala Thr Pro Ala Thr Gly			
225	230	235	240
Thr Gly Ser Lys Ala Gln Asp Thr Ala Arg Gly Lys Gly Lys Asp Ile			
245	250	255	
Ser Lys Tyr Gly Ser Val Gln Lys Ser Phe Ala Asp Arg Gly Leu Pro			
260	265	270	
Lys Pro Pro Lys Glu Lys Leu Leu Gln Val Glu Lys Leu Arg Lys Glu			
275	280	285	
Ser Gly Lys Gly Ser Phe Leu Gln Pro Thr Ala Lys Pro Arg Ala Leu			
290	295	300	
Ala Gln Gln Gln Ala Val Ile Arg Gly Phe Thr Tyr Tyr Lys Ala Gly			
305	310	315	320
Lys Gln Glu Val Thr Glu Ala Val Ala Asp Asn Thr Leu Gln Gly Thr			
325	330	335	
Ser Trp Leu Glu Gln Leu Pro Pro Lys Val Glu Gly Arg Ser Asn Ser			
340	345	350	
Ala Glu Pro Asn Ser Ala Glu Gln Asp Glu Ala Glu Pro Arg Ser Ser			
355	360	365	
Glu Arg Val Asp Leu Ala Ser Gly Thr Pro Thr Ser Ile Pro Ala Thr			
370	375	380	
Thr Thr Thr Ala Thr Thr Pro Thr Pro Thr Thr Ser Leu Leu Pro			
385	390	395	400
Thr Glu Pro Pro Ser Gly Pro Glu Val Ser Ser Gln Gly Arg Glu Ala			
405	410	415	
Ser Cys Glu Gly Thr Leu Arg Ala Val Asp Pro Pro Val Arg His His			
420	425	430	
Ser Tyr Gly Arg His Glu Gly Ala Trp Met Lys Asp Pro Ala Ala Arg			
435	440	445	
Asp Asp Arg Ile Tyr Val Thr Asn Tyr Tyr Gly Asn Ser Leu Val			
450	455	460	
Glu Phe Arg Asn Leu Glu Asn Phe Lys Gln Gly Arg Trp Ser Asn Met			
465	470	475	480
Tyr Lys Leu Pro Tyr Asn Trp Ile Gly Thr Gly His Val Val Tyr Gln			
485	490	495	
Gly Ala Phe Tyr Tyr Asn Arg Ala Phe Thr Lys Asn Ile Ile Lys Tyr			
500	505	510	
Asp Leu Arg Gln Arg Phe Val Ala Ser Trp Ala Leu Leu Pro Asp Val			
515	520	525	
Val Tyr Glu Asp Thr Thr Pro Trp Lys Trp Arg Gly His Ser Asp Ile			
530	535	540	
Asp Phe Ala Val Asp Glu Ser Gly Leu Trp Val Ile Tyr Pro Ala Val			
545	550	555	560

Asp Asp Arg Asp Glu Ala Gln Pro Glu Val Ile Val Leu Ser Arg Leu
 565 570 575
 Asp Pro Gly Asp Leu Ser Val His Arg Glu Thr Thr Trp Lys Thr Arg
 580 585 590
 Leu Arg Arg Asn Ser Tyr Gly Ash Cys Phe Leu Val Cys Gly Ile Leu
 595 600 605
 Tyr Ala Val Asp Thr Tyr Asn Gln Gln Glu Gly Gln Val Ala Tyr Ala
 610 615 620
 Phe Asp Thr His Thr Gly Thr Asp Ala Arg Pro Gln Leu Pro Phe Leu
 625 630 635 640
 Asn Glu His Ala Tyr Thr Thr Gln Ile Asp Tyr Asn Pro Lys Glu Arg
 645 650 655
 Val Leu Tyr Ala Trp Asp Asn Gly His Gln Leu Thr Tyr Thr Leu His
 660 665 670
 Phe Val Val
 675

<210> 268
 <211> 1909
 <212> DNA
 <213> Homo sapiens

<400> 268

gacacctttt	aaaatgcaga	actaacttag	gcatttcagt	aactttgttt	tcaaatcaat	60
aaagtcaaat	gtatggaaac	attttgtgcc	ctactctcca	taccctgtgt	actcaaattc	120
tctactgtat	gaatttatgt	ttaagtagaa	ttcagtggca	aggagaactt	ggtgaaataa	180
attattttaa	tttttttttt	atcccttaca	aagccatgg	tttttatttg	ttgatgtgt	240
ctctgtacac	aagccatttc	aataggatgg	agctgttaat	tatttccaa	agagtaatag	300
acatgcaaaa	gtttcaataa	aaactggggc	attaacaaat	aaattaataa	actaataaagc	360
atcccttct	agggttttgc	caaactgcct	atccaataac	aaatttgaga	atcggtgaaa	420
aagctagta	tatttcagag	aaatgatttt	cattattgaa	actgttctcc	ctagcaggcc	480
atttccctt	tttcctggg	gtttagcaag	tttaggagag	aatagtcatg	aaaagaaaagg	540
gaagaaaagg	gagaagggg	gaggttaaaa	agtaagtgc	cagacctatg	aacgtaatcc	600
ctttgctaga	aatatthaag	agcagctcg	cttgggttga	actgagttt	gtcatcttcc	660
atatttgcag	gaaggatttt	tctgacttgc	aatgcagcta	gatgtaaaat	tttattttat	720
catccctagaa	agccctgact	agaaaaatga	ataaaatattg	agggtttcct	gtccatatct	780
ggcttgcatt	tgccagaaag	cagagaatag	aaaatgtaat	ctccaacatc	caagcatcga	840
aacccaagg	gtaggcaatt	ctatgttagt	tttggacatg	aagtttgggt	catcttgggt	900
tatgctggct	caactgcatt	taaacctctc	tggcttata	tctcttcatt	ctattagaca	960
agcacgtatc	gaacacttgc	ttcgacaaag	gctctttagt	taacaattt	gcagctactg	1020
tttgcgttaa	acacactttt	caccaaata	gttctgaggc	aaacgagagc	aatgactatt	1080
taaagaaaagg	cttcccagc	atcaactaca	catccccaaa	ctaaaaagat	caactcttcc	1140
aactgagaaa	agactcctgg	cttgaatgg	aaacttacag	cagagagtca	caggccacgg	1200
caacaacaac	gacaacaaca	aacatttgg	atattattct	caactcacgt	ttaataata	1260
catcttaatt	atttttctag	tagagaaact	acaaatcagc	ctcttcaaca	tttatataca	1320
gtttaataag	cctcttgcaa	gttacttgg	ctctcacctg	aggatttttt	ttcctcccc	1380
ccttgcctt	gttctccct	tcctcttctc	ccttgcag	aggaaatatt	taacatattt	1440
gggtccaact	tcaataatgt	aataattaat	acattaaaag	catttaactt	cctttctaga	1500
aaaatgcaca	ggctaaggca	tagacaaaac	aaagagaaaat	gctgagaaaat	ttgccactgg	1560
agacaagcaa	tctgaataaa	tatttgc当地	aagttctttt	tatgtcatat	agtgtcagga	1620
tttgaaggag	ctatttttt	taatgttgca	actagcaact	catttcgga	agacacagcc	1680
aggagaatga	agtagaaatgt	aaagggtttat	aatccattt	gtaagcattt	atcccatata	1740
ttttaaaattc	aagaaaattt	gtgttatct	ttagaatttt	gtattcaata	ctttatgtac	1800
tatgtgactc	atgcttcgg	ataaataaaag	caccaatata	gtatctgtaa	ccacaaatcac	1860
acatattata	ttaaatatata	aaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1909

<210> 269
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 269

Met Tyr Gly Asn Ile Leu Cys Pro Thr Leu His Thr Leu Cys Thr Gln
 1 5 10 15
 Ile Leu Tyr Cys Met Asn Tyr Ala Leu Ser Arg Ile Gln Cys Gln Gly
 20 25 30
 Glu Leu Gly Glu Ile Asn Tyr Phe Asn Phe Phe Ile Leu Tyr Lys
 35 40 45
 Ala Met Asp Phe Ile Trp Leu Met Cys Ala Leu Tyr Thr Ser His Phe
 50 55 60
 Asn Arg Met Glu Leu Leu Ile Ile Phe Gln Arg Val Ile Asp Met Gln
 65 70 75 80
 Lys Phe Gln

<210> 270

<211> 1720

<212> DNA

<213> Homo sapiens

<400> 270

gactgcagat	gaaatttagta	actgggtgggg	tctgtgggtg	tgaatggtgg	gcgggagcag	60
ctatgtcagt	tgggtgtttt	ctgttatgt	tagggtaatt	ggcacggcc	tttgttaac	120
tgggtgaatat	ctctgaacct	gggcatgaaa	cagagagatg	tcctaactct	gggtgagagg	180
aatcctcatt	tttctctgcc	ctctcactgt	ggcatcctaa	aaaaaaagtt	ttgggttct	240
gcagccatgaa	ggagagctct	gctcccagaa	tttgggagct	ccagatttct	tccagggtgt	300
ggaggcatca	ataatatcagt	ctgggaaagg	ggttccttggg	ccactccagg	agctgagttg	360
ggtggaaggt	gctgagagtg	tgggtgggg	ccacttctga	gcacccatgt	ggcacccact	420
gctggccct	gtttgtgct	gggactcag	aaaaatgttt	ttggtgctaa	gagtaaaaag	480
ccaaccaaca	aacacatctc	tttttctgt	ctattcactg	gaaagtaaaa	gcagtctggg	540
cgcaggctgg	ggacccagat	ggaattcaaa	cttatgcctg	ctctcaaggt	gctcacggtt	600
gctgataaac	agctggataa	aatgaagagt	ctatgagtg	gggatgcaga	gccaggaaag	660
gctggtgag	tgtgccacc	agcacagggg	tatgagttt	cagctgccaa	ggggccaagg	720
gatgagctgg	ggccctcctt	cccaatggca	tctccctctg	gtctggaact	gaagacactg	780
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gagggtgtgg	agaatgcctg	cttccctca	gaggagcatg	agacccattt	ccagaaccct	900
gggaacacga	gactggcag	ctcacccagt	ccccctggg	gtgtctcctc	actgccccga	960
tcccagcggg	atgatctgc	ccttcattca	gaggaggggc	cagccctgga	gccccgtgagc	1020
cgcgggttgg	attatggctt	tgtttccgccc	ctcgtttcc	tggtgagtgg	gatttttctg	1080
gtggtgacag	catacgcct	ccccctgttag	gctcgagtca	atccggacac	agtgacagcg	1140
cgggagatgg	aacgactgga	gatgtactac	ccccccctag	gctcccacct	ggacaggtgc	1200
atcatcgccag	gcctcggct	gctcacggtg	ggcggcatgc	tcttgcgtt	gctgctcatg	1260
gtctccctgt	gcaagggcga	gcttaccgc	cggaggacct	tcttgcgtt	caagggctcc	1320
aggaagacct	acggctccat	taacctgcgc	atgagacagc	tcaatggga	tggggccag	1380
gccctgggtgg	agaatgaagt	tgtccaggct	tcagagacta	gccacaccct	ccagaggtct	1440
taagaacttag	cccacccctt	ctggctgttt	tagtccagg	gctacaagg	ccacccctgt	1500
ctcccgccca	cctgaccctt	gccaaggccc	tgggtttta	aactgagctc	acatagggcc	1560
tttgttggaaa	agtaactgggt	gctggaggg	gagctgggg	cccacccat	gccccacacg	1620
ggcaagcagc	ccactgatct	gttttgtagc	tgaggtttg	catacggtt	tgtttggagg	1680
atggcttctg	ctgctaaaaaa	tacaaaagtt	tggaaaccgc			1720

<210> 271

<211> 256

<212> PRT

<213> Homo sapiens

<400> 271

Met Pro Pro Ala Gln Gly Tyr Glu Phe Ala Ala Ala Lys Gly Pro Arg
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 Asp Glu Leu Gly Pro Ser Phe Pro Met Ala Ser Pro Pro Gly Leu Glu
 20 25 30
 Leu Lys Thr Leu Ser Asn Gly Pro Gln Ala Pro Arg Arg Ser Ala Pro

35	40	45													
Leu	Gly	Pro	Val	Ala	Pro	Thr	Arg	Glu	Gly	Val	Glu	Asn	Ala	Cys	Phe
50	55	60													
Ser	Ser	Glu	Glu	His	Glu	Thr	His	Phe	Gln	Asn	Pro	Gly	Asn	Thr	Arg
65	70	75	80												
Leu	Gly	Ser	Ser	Pro	Ser	Pro	Pro	Gly	Gly	Val	Ser	Ser	Leu	Pro	Arg
85	90	95													
Ser	Gln	Arg	Asp	Asp	Leu	Ser	Leu	His	Ser	Glu	Glu	Gly	Pro	Ala	Leu
100	105	110													
Glu	Pro	Val	Ser	Arg	Pro	Val	Asp	Tyr	Gly	Phe	Val	Ser	Ala	Leu	Val
115	120	125													
Phe	Leu	Val	Ser	Gly	Ile	Leu	Leu	Val	Val	Thr	Ala	Tyr	Ala	Ile	Pro
130	135	140													
Arg	Glu	Ala	Arg	Val	Asn	Pro	Asp	Thr	Val	Thr	Ala	Arg	Glu	Met	Glu
145	150	155	160												
Arg	Leu	Glu	Met	Tyr	Tyr	Ala	Arg	Leu	Gly	Ser	His	Leu	Asp	Arg	Cys
165	170	175													
Ile	Ile	Ala	Gly	Leu	Gly	Leu	Leu	Thr	Val	Gly	Gly	Met	Leu	Leu	Ser
180	185	190													
Val	Leu	Leu	Met	Val	Ser	Leu	Cys	Lys	Gly	Glu	Leu	Tyr	Arg	Arg	Arg
195	200	205													
Thr	Phe	Val	Pro	Gly	Lys	Gly	Ser	Arg	Lys	Thr	Tyr	Gly	Ser	Ile	Asn
210	215	220													
Leu	Arg	Met	Arg	Gln	Leu	Asn	Gly	Asp	Gly	Gly	Gln	Ala	Leu	Val	Glu
225	230	235	240												
Asn	Glu	Val	Val	Gln	Val	Ser	Glu	Thr	Ser	His	Thr	Leu	Gln	Arg	Ser
245	250	255													

<210> 272

<211> 1111

<212> DNA

<213> Homo sapiens

<400> 272

ccgcgcgctc	ccccggccgc	tcctgctgca	ccccaggccc	cctcgccgcc	gccaccatgg	60
acgcacatcaa	gaagaagatg	cagatgctga	agctcgacaa	ggagaacgccc	ttggatcgag	120
ctgagcaggc	ggaggccgac	aagaaggcgg	cggaagacag	gagcaaggcag	ctgaaagatg	180
agctgggtgc	actgaaaaag	aaactcaagg	gcaccgaaga	tgaactggac	aaatactctg	240
aggctctcaa	agatgcccag	gagaagctgg	agctggcaga	aaaaaaggcc	accgatgtcg	300
aagccgacgt	agcttctctg	aacagacgca	tccagctgtt	tgaggaagag	ttggatctgt	360
cccaggagcg	tctggcaaca	gctttgcaga	agctggagga	agctgagaag	gcagcagatg	420
agagttagag	aggcatgaaa	gtcattgaga	gtcgagccca	aaaagatgaa	aaaaaatgg	480
aaattcagga	gatccaactg	aaagaggcca	agcacatgc	tgaagatgcc	gaccgcaat	540
acgaagaggt	ggcccgtaag	ctggcatca	ttgagagcga	cctggaacgt	gcagaggagc	600
gggctgagct	ctcagaaggc	aatatgtccg	agcttgaaga	agaattgaaa	actgtgacga	660
acaacttcaa	gtcactggag	gctcaggctg	agaagtactc	gcagaaggaa	gacagatatg	720
aggaagagat	caaggtcctt	tccgacaagc	tgaaggaggc	tgagactcgg	gctgagttg	780
cgagaggtc	agtaactaaa	ttggagaaaa	gcattgtga	cttagaagac	gagctgtacg	840
ctcagaaact	gaagtacaaa	gccatcagcg	aggagctgg	ccacgctctc	aacgatatga	900
cttccatata	agtttctttg	cttcacttct	cccaagactc	cctcgtcgag	ctggatgtcc	960
cacctctctg	agctctgcat	ttgtctattc	tccagctgac	cctgggtctc	tctcttagca	1020
tcctgcctta	gagccaggca	cacactgtgc	tttcttatgt	acagaagctc	ttcgtttcag	1080
tgtcaaataa	acactgtga	agctaaaaaa	a			1111

<210> 273

<211> 284

<212> PRT

<213> Homo sapiens

<400> 273

Met Asp Ala Ile Lys Lys Lys Met Gln Met Leu Lys Leu Asp Lys Glu

1	5	10	15												
Asn	Ala	Leu	Asp	Arg	Ala	Glu	Gln	Ala	Glu	Ala	Asp	Lys	Lys	Ala	Ala
			20			25					30				
Glu	Asp	Arg	Ser	Lys	Gln	Leu	Glu	Asp	Glu	Leu	Val	Ser	Leu	Gln	Lys
			35			40					45				
Lys	Leu	Lys	Gly	Thr	Glu	Asp	Glu	Leu	Asp	Lys	Tyr	Ser	Glu	Ala	Leu
			50			55					60				
Lys	Asp	Ala	Gln	Glu	Lys	Leu	Glu	Leu	Ala	Glu	Lys	Lys	Ala	Thr	Asp
			65			70				75				80	
Ala	Glu	Ala	Asp	Val	Ala	Ser	Leu	Asn	Arg	Arg	Ile	Gln	Leu	Val	Glu
			85			90					95				
Glu	Glu	Leu	Asp	Arg	Ala	Gln	Glu	Arg	Leu	Ala	Thr	Ala	Leu	Gln	Lys
			100			105					110				
Leu	Glu	Glu	Ala	Glu	Lys	Ala	Ala	Asp	Glu	Ser	Glu	Arg	Gly	Met	Lys
			115			120					125				
Val	Ile	Glu	Ser	Arg	Ala	Gln	Lys	Asp	Glu	Glu	Lys	Met	Glu	Ile	Gln
			130			135					140				
Glu	Ile	Gln	Leu	Lys	Glu	Ala	Lys	His	Ile	Ala	Glu	Asp	Ala	Asp	Arg
			145			150					155				160
Lys	Tyr	Glu	Glu	Val	Ala	Arg	Lys	Leu	Val	Ile	Ile	Glu	Ser	Asp	Leu
			165			170					175				
Glu	Arg	Ala	Glu	Glu	Arg	Ala	Glu	Leu	Ser	Glu	Gly	Lys	Cys	Ala	Glu
			180			185					190				
Leu	Glu	Glu	Leu	Lys	Thr	Val	Thr	Asn	Asn	Leu	Lys	Ser	Leu	Glu	
			195			200					205				
Ala	Gln	Ala	Glu	Lys	Tyr	Ser	Gln	Lys	Glu	Asp	Arg	Tyr	Glu	Glu	
			210			215					220				
Ile	Lys	Val	Leu	Ser	Asp	Lys	Leu	Lys	Glu	Ala	Glu	Thr	Arg	Ala	Glu
			225			230					235				240
Phe	Ala	Glu	Arg	Ser	Val	Thr	Lys	Leu	Glu	Lys	Ser	Ile	Asp	Asp	Leu
			245			250					255				
Glu	Asp	Glu	Leu	Tyr	Ala	Gln	Lys	Leu	Lys	Tyr	Lys	Ala	Ile	Ser	Glu
			260			265					270				
Glu	Leu	Asp	His	Ala	Leu	Asn	Asp	Met	Thr	Ser	Ile				
			275			280									

<210> 274

<211> 2032

<212> DNA

<213> Homo sapiens

<400> 274

caccccgccag	ccccggcctcg	gcctccgccc	cttgggttcg	cgccccggcc	gcgagcccg	60
cccgcacgtc	ccccggccggc	ggccaccatg	agcacaggcc	tgcggtacaa	gagcaagctg	120
gcgcaccccg	aggacaagca	ggacattgc	aagcagtacg	tggcttcgc	cacactgccc	180
aaccagggtc	accgcaagtc	ggtgaagaaa	ggctttgact	tcacactcat	ggtggcttgt	240
gagtcaggcc	tggggaaatc	cacactggtc	cacagccctt	tcctgacaga	tttgtacaag	300
gaccggaaatc	tgctcagtc	tgaggagcgc	atcagccaga	cggttagagat	tctaaaacac	360
acgggtggaca	ttgaggagaa	gggagtcaag	ctgaagctca	ccatcgtgga	cacgcccggga	420
ttcggggacg	ctgtcaacaa	caccgagtgc	tggaagccca	tcacccgacta	tgtggaccag	480
cagtttgagc	agtacttccg	tgtgagagc	ggcctcaacc	gaaagaacat	ccaagacaac	540
cgagtgcact	gctgcctata	tttcatctcc	cccttcgggc	atgggctgcg	gccagtggat	600
gtgggtttca	tgaaggcatt	gcatgagaag	gtcaacatcg	tgccctctcat	cgccaaagct	660
gactgtcttg	tccccagtg	gatccggaag	ctgaaggagc	ggatccggga	ggagattgac	720
aagtttggga	tccatgtata	ccagttccct	gagtgtact	cgagcaggg	tgaggacttc	780
aagcagcagg	accgggaact	gaaggagagc	gcgccttcg	ccgttatagg	cagcaacacg	840
gtggggggc	ccaaaggggca	gcgggtccgg	ggccgactgt	accctgggg	gatcgtggag	900
gtggagaacc	aggcgcatcg	cgacttcgt	aagctgcga	acatgctcat	ccgcacgcac	960
atgcacgacc	tcaaggacgt	gacgtgcgc	gtgcactacg	agaactaccg	cgcgactgc	1020
atccagcaga	tgaccagcaa	actgaccagg	gacagccgca	tggagagccc	catccccatc	1080
ctgcccgtgc	ccaccccgga	cgccgagact	gagaagctta	tcaggatgaa	ggatgaggaa	1140

ctgaggcgca	tgcaggagat	gctgcagagg	atgaagcagc	agatgcagga	ccagtgcacgc	1200
tcgcccggaa	cacaccgtcc	gtctccggga	cgccctcgca	cccctggaca	ccagaccggaa	1260
ctgttcccgaa	ccccggagacg	cggggccaca	gcccccaact	gaccctaatt	tatttctcagc	1320
accacccctt	cccaggtcat	tgtgtctgtt	tccgaggggc	ctggaccgt	gccccccgccc	1380
agctggccct	ctctgaccc	ggggatcag	gagcgaagtt	ggggggact	ttagagatcc	1440
gcctcccttg	cccttcccccc	gccccccggac	ggtcacagca	cccaaaccgc	aggcccgtct	1500
ctggcaggca	ggcaaagcta	ggcagaagag	gattcccagg	atcctgggtc	tgttccctgc	1560
cccagtctg	cagaacggac	ttgggagccc	tcctttgcct	gctcccgccg	gtcacccagc	1620
gagtgtctgag	accccatttt	ctgtcgaggc	ggggccgagtc	ttcccttatac	cccagacgcc	1680
tagccggcag	ggttgggctg	aatccaaatgg	gagcccttcca	gacataagga	ggccagaggc	1740
tgcaaggagc	ggggtcgtga	ccgcattacac	cccttcttcca	cagcccgcc	cgacctggag	1800
ggccccccgg	gcactgggctg	gtgagccacc	tcctggcaac	tetcgggtc	gtcccctgccc	1860
ctcgctcgag	gccttttctc	cccagcaccg	ctgtgggtgt	ccgggatct	gagccttaggc	1920
ctcccgatgt	tcccacccgc	atgatccctt	cccgccacac	gatgctccgt	tttcttcgt	1980
tgtgaatgcc	gcgtcctgtc	ctggtgacag	gagaacaatg	ttggtaacg	tc	2032

<210> 275

<211> 369

<212> PRT

<213> Homo sapiens

<400> 275

Met	Ser	Thr	Gly	Leu	Arg	Tyr	Lys	Ser	Lys	Leu	Ala	Thr	Pro	Glu	Asp
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Lys	Gln	Asp	Ile	Asp	Lys	Gln	Tyr	Val	Gly	Phe	Ala	Thr	Leu	Pro	Asn
							20		25			30			
Gln	Val	His	Arg	Lys	Ser	Val	Lys	Lys	Gly	Phe	Asp	Phe	Thr	Leu	Met
							35		40			45			
Val	Ala	Gly	Glu	Ser	Gly	Leu	Gly	Lys	Ser	Thr	Leu	Val	His	Ser	Leu
	50					55					60				
Phe	Leu	Thr	Asp	Leu	Tyr	Lys	Asp	Arg	Lys	Leu	Leu	Ser	Ala	Glu	Glu
	65					70				75			80		
Arg	Ile	Ser	Gln	Thr	Val	Glu	Ile	Leu	Lys	His	Thr	Val	Asp	Ile	Glu
						85			90			95			
Glu	Lys	Gly	Val	Lys	Leu	Lys	Leu	Thr	Ile	Val	Asp	Thr	Pro	Gly	Phe
	100						105				110				
Gly	Asp	Ala	Val	Asn	Asn	Thr	Glu	Cys	Trp	Lys	Pro	Ile	Thr	Asp	Tyr
	115						120				125				
Val	Asp	Gln	Gln	Phe	Glu	Gln	Tyr	Phe	Arg	Asp	Glu	Ser	Gly	Leu	Asn
	130					135				140					
Arg	Lys	Asn	Ile	Gln	Asp	Asn	Arg	Val	His	Cys	Cys	Leu	Tyr	Phe	Ile
	145					150				155			160		
Ser	Pro	Phe	Gly	His	Gly	Leu	Arg	Pro	Val	Asp	Val	Gly	Phe	Met	Lys
						165			170			175			
Ala	Leu	His	Glu	Lys	Val	Asn	Ile	Val	Pro	Leu	Ile	Ala	Lys	Ala	Asp
	180						185				190				
Cys	Leu	Val	Pro	Ser	Glu	Ile	Arg	Lys	Leu	Lys	Glu	Arg	Ile	Arg	Glu
	195						200				205				
Glu	Ile	Asp	Lys	Phe	Gly	Ile	His	Val	Tyr	Gln	Phe	Pro	Glu	Cys	Asp
	210					215				220					
Ser	Asp	Glu	Asp	Glu	Asp	Phe	Lys	Gln	Gln	Asp	Arg	Glu	Leu	Lys	Glu
	225					230				235			240		
Ser	Ala	Pro	Phe	Ala	Val	Ile	Gly	Ser	Asn	Thr	Val	Val	Glu	Ala	Lys
						245				250			255		
Gly	Gln	Arg	Val	Arg	Gly	Arg	Leu	Tyr	Pro	Trp	Gly	Ile	Val	Glu	Val
	260					265					270				
Glu	Asn	Gln	Ala	His	Cys	Asp	Phe	Val	Lys	Leu	Arg	Asn	Met	Leu	Ile
	275					280					285				
Arg	Thr	His	Met	His	Asp	Leu	Lys	Asp	Val	Thr	Cys	Asp	Val	His	Tyr
	290					295					300				
Glu	Asn	Tyr	Arg	Ala	His	Cys	Ile	Gln	Gln	Met	Thr	Ser	Lys	Leu	Thr

305	310	315	320
Gln Asp Ser Arg Met Glu Ser Pro Ile Pro Ile Leu Pro Leu Pro Thr			
325	330	335	
Pro Asp Ala Glu Thr Glu Lys Leu Ile Arg Met Lys Asp Glu Glu Leu			
340	345	350	
Arg Arg Met Gln Glu Met Leu Gln Arg Met Lys Gln Gln Met Gln Asp			
355	360	365	
Gln			

<210> 276
<211> 1344
<212> DNA
<213> Homo sapiens

<400> 276

tgcagactga tatggattca ccactgctaa cacccctgg ttggaactac aggaatagaa	60
ctggaaaaggg aaaaaaggca gcattcacca catcccaatc ctgaatccaa gagtctaaga	120
tagtccccca ctcctatctc aggcttagag gattagatta atccctggg gggaaagactc	180
ttccttgaaa cattttttt tattctgcctg tagctattgg gataattcg gaaatccaca	240
gggacagttc aagtcatctt tgccctctac tttctgttgc actctcagcc ttgttctt	300
tttagaaaact gcatggtaac tattatata tagctaaaga gcatctgac ctctgcctg	360
ggacttcctg gatcctcctc ttcttataaa tacaaggca gagctggat cccggggagc	420
caggaagcag tgagcccagg agtcctcggc cagccctgcc tgcccaccag gaggatgaa	480
gtctccgtgg ctgcctctc ctgcctcatg ctttgttgc tccttggatc ccaggcccag	540
ttcacaaaatg atgcagagac agagttaatg atgtcaaaagc ttccactggaa aaatccagta	600
gttctgaaca gcttcactt tgctgctgac tgctgcacct cctacatctc acaaagcatc	660
ccgtgttcac tcatgaaaat ttatTTGAA acgagcagcg agtgctccaa gccagggtgc	720
atattcctca ccaagaaggc gcgcaagtc tggccaaac ccagtggatc gggagttcag	780
gattgcatga aaaagctgaa gcctactca atataataat aaagagacaa aagaggccag	840
ccacccaccc ccaacacctc ctgagccctc gaagctccca ccaggccagc tctcctccca	900
caacagcttc ccacagcatg aagatctccg tggctccat tcccttctc ctccatca	960
ccatcgccct agggaccaag actgaatcc ctcacgggg accttaccac ccctcagagt	1020
gctgttccac ctacactacc tacaagatcc cgctcagcg gattatggat tactatgaga	1080
ccaacagcca gtgctccaaag cccggaaattg tcttcatcac caaaaggggc cattccgtct	1140
gtaccaaccc cagtgacaag tgggtccagg actatatcaa ggacatgaa gagaactgag	1200
tgacccagaa ggggtggcga aggacacagct cagagacata aagagaagat gccaaggccc	1260
cctcctccac ccacgcctaa ctctcagccc cagtcaccct cttggagctt ccctgcttg	1320
aattaaagac cactcatgt ctcc	1344

<210> 277

<211> 93
<212> PRT
<213> Homo sapiens

<400> 277

Met Lys Ile Ser Val Ala Ala Ile Pro Phe Phe Leu Leu Ile Thr Ile	
1 5 10 15	
Ala Leu Gly Thr Lys Thr Glu Ser Ser Ser Arg Gly Pro Tyr His Pro	
20 25 30	
Ser Glu Cys Cys Phe Thr Tyr Thr Thr Tyr Lys Ile Pro Arg Gln Arg	
35 40 45	
Ile Met Asp Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile	
50 55 60	
Val Phe Ile Thr Lys Arg Gly His Ser Val Cys Thr Asn Pro Ser Asp	
65 70 75 80	
Lys Trp Val Gln Asp Tyr Ile Lys Asp Met Lys Glu Asn	
85 90	

<210> 278

<211> 1344

<212> DNA
 <213> Homo sapiens

<400> 278

tgcagactga	tatggattca	ccactgctaa	cacccctgg	ttggaactac	aggaataaaaa	60
ctggaaaagg	aaaaaaaggca	gcattcacca	catcccaatc	ctgaatccaa	gagtctaaga	120
tagtccccca	ctccttatc	aggcttagag	gattagatta	atccctgg	ggaaagactc	180
ttccttgaaa	cattttttt	tatctgcctg	tagctattgg	gataattcg	aaaatccaca	240
gggacagttc	aagtcatctt	tgtcctctac	tttctgtgc	actctcagcc	ttgttctt	300
tttagaaact	gcatggtaac	tattatata	ctaaagaaga	gcattctgac	ctctgcctg	360
ggacttcctg	gatcctc	ttcttataaa	tacaaggca	gagctggat	ccgggggagc	420
caggaagcag	tgagcccagg	agtctcgcc	cagccctg	tgcccaccag	gaggatgaag	480
gtctccgtgg	ctgccc	ctgcctcatg	tttgttgc	tccttggatc	ccaggccccag	540
ttcacaaatg	atgcagagac	agagttatg	atgtcaaagc	ttcactgg	aaatccagta	600
gttctgaaca	gctttactt	tgctgctgac	tgctgcac	cctacatc	acaaagcata	660
ccgtgttac	tcatgaaaag	ttatttgaa	acgagcagcg	agtctccaa	gccagggtgc	720
atattccctca	ccaagaagg	gcccgaatc	tgtccaaac	ccagtgg	gggagtttag	780
gattgcatga	aaaagctaa	gcctactca	atataataat	aaaqagacaa	aagaggccag	840
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caacagctc	ccacagcatg	aagatctcg	tggctgc	ccatccatca	ccatccatca	960
ccatcgccct	agggaccaag	actgaatc	cctcacggg	acccatccac	ccctcagagt	1020
gctgttac	ctacactacc	tacaagatcc	cgcgtcagcg	gattatggat	tactatgaga	1080
ccaaacagcc	gtgctccaa	cccgaaattg	tcttcatcac	caaaagg	catccgtct	1140
gtaccaaccc	cagtgacaag	tggtccagg	actatataa	ggacatgaag	gagaactgag	1200
tgacccagaa	gggggtggc	aggcacagct	cagagacata	aagagaagat	gccaaggccc	1260
cctctccac	ccaccgctaa	ctctcagccc	cagtcaccc	tttggagctt	ccctgctt	1320
aattaaagac	cactcatgct	cttc				1344

<210> 279
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 279

Met	Lys	Ile	Ser	Val	Ala	Ala	Ile	Pro	Phe	Phe	Leu	Leu	Ile	Thr	Ile
1				5				10					15		
Ala	Leu	Gly	Thr	Lys	Thr	Glu	Ser	Ser	Ser	Arg	Gly	Pro	Tyr	His	Pro
					20			25					30		
Ser	Glu	Cys	Cys	Phe	Thr	Tyr	Thr	Thr	Tyr	Lys	Ile	Pro	Arg	Gln	Arg
						35		40			45				
Ile	Met	Asp	Tyr	Tyr	Glu	Thr	Asn	Ser	Gln	Cys	Ser	Lys	Pro	Gly	Ile
	50				55				60						
Val	Phe	Ile	Thr	Lys	Arg	Gly	His	Ser	Val	Cys	Thr	Asn	Pro	Ser	Asp
65					70				75				80		
Lys	Trp	Val	Gln	Asp	Tyr	Ile	Lys	Asp	Met	Lys	Glu	Asn			
					85				90						

<210> 280
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<400> 280

tgcagactga	tatggattca	ccactgctaa	cacccctgg	ttggaactac	aggaataaaaa	60
ctggaaaagg	aaaaaaaggca	gcattcacca	catcccaatc	ctgaatccaa	gagtctaaga	120
tagtccccca	ctccttatc	aggcttagag	gattagatta	atccctgg	ggaaagactc	180
ttccttgaaa	cattttttt	tatctgcctg	tagctattgg	gataattcg	aaaatccaca	240
gggacagttc	aagtcatctt	tgtcctctac	tttctgtgc	actctcagcc	ttgttctt	300
tttagaaact	gcatggtaac	tattatata	ctaaagaaga	gcattctgac	ctctgcctg	360
ggacttcctg	gatcctc	ttcttataaa	tacaaggca	gagctggat	ccgggggagc	420
caggaagcag	tgagcccagg	agtctcgcc	cagccctg	tgcccaccag	gaggatgaag	480

gtctccgtgg	ctgcccttc	ctgcctcatg	cttggatc	ttccatggatc	ccaggcccag	540
ttcacaaatg	atgcagagac	agagttaatg	atgtcaaagc	ttccactgga	aaatccagta	600
gttctgaaca	gcttcactt	tgctgctgac	tgctgcacct	cctacatctc	acaaaagcatc	660
ccgtgttcac	tcatgaaaaag	ttatttgaa	acgagcagcg	agtgcctcaa	gccagggttc	720
atattcctca	ccaagaaggg	gcccgaatgc	tgtgccaac	ccagtggtcc	gggagtttag	780
gattgcatga	aaaagctgaa	gcctactca	atataataat	aaagagacaa	aagagggcag	840
ccacccacct	ccaacaccc	ctgagcctct	gaagctccca	ccaggccagc	tctcctccca	900
caacagcttc	ccacagcatg	aagatctccg	tggctgcccc	tcccttcttc	ctcctcatca	960
ccatcgccct	agggaccaag	actgaatctt	cctcacgggg	accttaccac	ccctcagagt	1020
gctgcttcac	ctacactacc	tacaagatcc	cgcgtcagcg	gattatggat	tactatgaga	1080
ccaacagcca	gtgctccaaag	cccgaaattg	tcttcatcac	caaaaggggc	cattccgtct	1140
gtaccaaccc	cagtgacaag	tgggtccagg	actatataaa	ggacatgaag	gagaactgag	1200
tgacccagaa	gggggtggcga	aggcacagct	cagagacata	aaagagaagat	gc当地agccc	1260
cctcctccac	ccaccgctaa	ctctcagccc	cagtcaccct	cttggagctt	ccctgctttg	1320
aattaaagac	cactcatgct	cttc				1344

<210> 281

<211> 93

<212> PRT

<213> Homo sapiens

<400> 281

Met	Lys	Ile	Ser	Val	Ala	Ala	Ile	Pro	Phe	Phe	Leu	Leu	Ile	Thr	Ile
1					5				10				15		
Ala	Leu	Gly	Thr	Lys	Thr	Glu	Ser	Ser	Ser	Arg	Gly	Pro	Tyr	His	Pro
							20		25				30		
Ser	Glu	Cys	Cys	Phe	Thr	Tyr	Thr	Thr	Tyr	Lys	Ile	Pro	Arg	Gln	Arg
							35		40			45			
Ile	Met	Asp	Tyr	Tyr	Glu	Thr	Asn	Ser	Gln	Cys	Ser	Lys	Pro	Gly	Ile
							50		55			60			
Val	Phe	Ile	Thr	Lys	Arg	Gly	His	Ser	Val	Cys	Thr	Asn	Pro	Ser	Asp
							65		70			75			80
Lys	Trp	Val	Gln	Asp	Tyr	Ile	Lys	Asp	Met	Lys	Glu	Asn			
							85			90					

<210> 282

<211> 2750

<212> DNA

<213> Homo sapiens

<400> 282

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atcgccgcgg	ccaaggccct	gctggcgtgg	ctggaccgat	tgctatTTTA	tgtgtcaTTT	120
gagagaaaac	agttaataaa	aaactaattt	aatacAAAAT	ttagctgggc	ttgggtggcac	180
atgcctgtaa	tcccagctac	tcggaggct	gaagcaggag	agtgcTTGA	acctgggagg	240
cgttagattgc	agtgagccaa	gatcatccca	ctgcactcca	gcctggcga	cagagtgaga	300
cacagtctca	aacaaaacaa	aacaaaaagg	aatttagAGT	agccatGGG	gtagctatgc	360
ttaccaacat	ccagtggat	ccccgtggat	tctccctacc	ccttttaag	aggattttg	420
ctaccttcta	gggctccgtt	tacagggtac	actgatttct	cagtcacgaa	gaacaaaatt	480
atccagcttt	gcttggacct	gaccactaca	gtccagaagg	attgtttgt	agcggaaatg	540
gaggataaaag	tttttaactgt	ggtaagggtt	ttaaatggca	tctgtgacaa	aacaatccga	600
tctaccacag	atcctgtgt	gagccagtgt	gcatgtctgg	aggaagttca	cttaccaaacc	660
attaaacctg	gggaaggcct	gggcatgtac	atcaaataaa	cctatgtatgg	gttacacgtg	720
attactggaa	ccacagaaaa	ttctcctgca	gacagatctc	agaagattca	tgctggtgac	780
gaagtcatTC	aagttaatca	gcaactgtg	gtgggatggc	agctgaaaaaa	tctgtgaaag	840
aaatttgagag	agaatccac	cgaggttgtg	ttactgctta	agaagcgcCc	caccgggtct	900
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<212> PRT
<213> *Homo sapiens*

<220>
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<400> 283

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Cys Leu Glu Glu Val His Leu Pro Asn Ile Lys Pro Gly Glu Gly Leu
   35          .          40          45
Gly Met Tyr Ile Lys Ser Thr Tyr Asp Gly Leu His Val Ile Thr Gly
   50          .          55          60
Thr Thr Glu Asn Ser Pro Ala Asp Arg Ser Gln Lys Ile His Ala Gly
   65          .          70          75          80
Asp Glu Val Ile Gln Val Asn Gln Gln Thr Val Val Gly Trp Gln Leu
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Lys Asn Leu Val Lys Lys Leu Arg Glu Asn Pro Thr Gly Val Val Leu
  100          .          105          110
Leu Leu Lys Lys Arg Pro Thr Gly Ser Phe Asn Phe Thr Pro Ala Pro
  115          .          120          125
Leu Lys Asn Leu Arg Trp Lys Pro Pro Leu Val Gln Thr Ser Pro Pro
  130          .          135          140
Pro Ala Thr Thr Gln Ser Pro Glu Ser Thr Met Asp Thr Ser Leu Lys
  145          .          150          155          160
Lys Glu Lys Ser Ala Ile Leu Asp Leu Tyr Ile Pro Pro Pro Pro Ala
  165          .          170          175
Val Pro Tyr Ser Pro Arg Asp Glu Asn Gly Ser Phe Val Tyr Gly Gly

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Pro	Thr	Lys	Met	Arg	Glu	Lys	Thr	Pro	Ser	Tyr	Xaa	Lys	Pro	Arg	Pro
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Leu	Ser	Met	Pro	Ala	Asp	Gly	Asn	Trp	Met	Gly	Ile	Val	Asp	Pro	Phe
				260		265					270				
Ala	Arg	Pro	Arg	Gly	His	Gly	Arg	Lys	Gly	Glu	Asp	Ala	Leu	Cys	Arg
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Tyr	Phe	Ser	Asn	Glu	Arg	Ile	Pro	Pro	Ile	Ile	Glu	Glu	Ser	Ser	Ser
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				295							300				
Pro	Pro	Tyr	Arg	Phe	Ser	Arg	Pro	Thr	Thr	Glu	Arg	His	Leu	Val	Arg
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				310						315			320		
Gly	Ala	Asp	Tyr	Ile	Arg	Gly	Ser	Arg	Cys	Tyr	Ile	Asn	Ser	Asp	Leu
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His	Ser	Ser	Ala	Thr	Ile	Pro	Phe	Gln	Glu	Gly	Thr	Lys	Lys	Lys	
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Ser	Gly	Ser	Ser	Ala	Thr	Lys	Ser	Ser	Ser	Thr	Glu	Pro	Ser	Leu	Leu
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<210> 284

<211> 1789

<212> DNA

<213> Homo sapiens

<400> 284

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<210> 285

<211> 335

<212> PRT

<213> Homo sapiens

<400> 285

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Pro	Lys	Ile	Leu	Arg	Gln	Leu	Gly	Ser	Lys	Val	Leu	Leu	Pro	Leu	Thr
						35		40						45	
Tyr	Glu	Arg	Ile	Asn	Lys	Ser	Met	Asn	Lys	Ser	Ile	His	Ile	Val	Val
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Thr	Met	Ala	Lys	Ser	Leu	Glu	Asn	Ser	Val	Glu	Asn	Lys	Ile	Val	Ser
						65		70		75				80	
Leu	Asp	Pro	Ser	Glu	Ala	Gly	Pro	Pro	Arg	Tyr	Leu	Gly	Asp	Arg	Tyr
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Lys	Phe	Tyr	Leu	Glu	Asn	Leu	Thr	Leu	Gly	Ile	Arg	Glu	Ser	Arg	Lys
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Glu	Asp	Glu	Gly	Trp	Tyr	Leu	Met	Thr	Leu	Glu	Lys	Asn	Val	Ser	Val
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Gln	Arg	Phe	Cys	Leu	Gln	Leu	Arg	Leu	Tyr	Glu	Gln	Val	Ser	Thr	Pro
						130			135					140	
Glu	Ile	Lys	Val	Leu	Asn	Lys	Thr	Gln	Glu	Asn	Gly	Thr	Cys	Thr	Leu
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Ile	Leu	Gly	Cys	Thr	Val	Glu	Lys	Gly	Asp	His	Val	Ala	Tyr	Ser	Trp
						165			170					175	
Ser	Glu	Lys	Ala	Gly	Thr	His	Pro	Leu	Asn	Pro	Ala	Asn	Ser	Ser	His
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Leu	Leu	Ser	Leu	Thr	Leu	Gly	Pro	Gln	His	Ala	Asp	Asn	Ile	Tyr	Ile
						195			200					205	
Cys	Thr	Val	Ser	Asn	Pro	Ile	Ser	Asn	Asn	Ser	Gln	Thr	Phe	Ser	Pro
						210		215						220	
Trp	Pro	Gly	Cys	Arg	Thr	Asp	Pro	Ser	Glu	Thr	Lys	Pro	Trp	Ala	Val
						225		230		235				240	
Tyr	Ala	Gly	Leu	Leu	Gly	Gly	Val	Ile	Met	Ile	Leu	Ile	Met	Val	Val
						245			250					255	
Ile	Leu	Gln	Leu	Arg	Arg	Gly	Lys	Thr	Asn	His	Tyr	Gln	Thr	Thr	
						260			265					270	
Val	Glu	Lys	Lys	Ser	Leu	Thr	Ile	Tyr	Ala	Gln	Vai	Gln	Lys	Pro	Gly
						275			280					285	
Pro	Leu	Gln	Lys	Lys	Leu	Asp	Ser	Phe	Pro	Ala	Gln	Asp	Pro	Cys	Thr
						290		295						300	
Thr	Ile	Tyr	Val	Ala	Ala	Thr	Glu	Pro	Val	Pro	Glu	Ser	Val	Gln	Glu
						305		310		315				320	
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<210> 286

<211> 305

<212> PRT

<213> Homo sapiens

<400> 286

Met	Asp	Pro	Lys	Gly	Leu	Leu	Ser	Leu	Thr	Phe	Val	Leu	Phe	Leu	Ser
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						20		25						30	

Pro Lys Ile Leu Arg Gln Leu Gly Ser Lys Val Leu Leu Pro Leu Thr
 35 40 45
 Tyr Glu Arg Ile Asn Lys Ser Met Asn Lys Ser Ile His Ile Val Val
 50 55 60
 Thr Met Ala Lys Ser Leu Glu Asn Ser Val Glu Asn Lys Ile Val Ser
 65 70 75 80
 Leu Asp Pro Ser Glu Ala Gly Pro Pro Arg Tyr Leu Gly Asp Arg Tyr
 85 90 95
 Lys Phe Tyr Leu Glu Asn Leu Thr Leu Gly Ile Arg Glu Ser Arg Lys
 100 105 110
 Glu Asp Glu Gly Trp Tyr Leu Met Thr Leu Glu Lys Asn Val Ser Val
 115 120 125
 Gln Arg Phe Cys Leu Gln Leu Arg Leu Tyr Glu Gln Val Ser Thr Pro
 130 135 140
 Glu Ile Lys Val Leu Asn Lys Thr Gln Glu Asn Gly Thr Cys Thr Leu
 145 150 155 160
 Ile Leu Gly Cys Thr Val Glu Lys Gly Asp His Val Ala Tyr Ser Trp
 165 170 175
 Ser Glu Lys Ala Gly Thr His Pro Leu Asn Pro Ala Asn Ser Ser His
 180 185 190
 Leu Leu Ser Leu Thr Leu Gly Pro Gln His Ala Asp Asn Ile Tyr Ile
 195 200 205
 Cys Thr Val Ser Asn Pro Ile Ser Asn Asn Ser Gln Thr Phe Ser Pro
 210 215 220
 Trp Pro Gly Cys Arg Thr Asp Pro Ser Gly Lys Thr Asn His Tyr Gln
 225 230 235 240
 Thr Thr Val Glu Lys Lys Ser Leu Thr Ile Tyr Ala Gln Val Gln Lys
 245 250 255
 Pro Gly Pro Leu Gln Lys Lys Leu Asp Ser Phe Pro Ala Gln Asp Pro
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 Ser
 305

<210> 287
 <211> 298
 <212> PRT
 <213> Homo sapiens

<400> 287
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 35 40 45
 Tyr Glu Arg Ile Asn Lys Ser Met Asn Lys Ser Ile His Ile Val Val
 50 55 60
 Thr Met Ala Lys Ser Leu Glu Asn Ser Val Glu Asn Lys Ile Val Ser
 65 70 75 80
 Leu Asp Pro Ser Glu Ala Gly Pro Pro Arg Tyr Leu Gly Asp Arg Tyr
 85 90 95
 Lys Phe Tyr Leu Glu Asn Leu Thr Leu Gly Ile Arg Glu Ser Arg Lys
 100 105 110
 Glu Asp Glu Gly Trp Tyr Leu Met Thr Leu Glu Lys Asn Val Ser Val
 115 120 125
 Gln Arg Phe Cys Leu Gln Leu Arg Leu Tyr Glu Gln Val Ser Thr Pro
 130 135 140

Glu Ile Lys Val Leu Asn Lys Thr Gln Glu Asn Gly Thr Cys Thr Leu
 145 150 155 160
 Ile Leu Gly Cys Thr Val Glu Lys Gly Asp His Val Ala Tyr Ser Trp
 165 170 175
 Ser Glu Lys Ala Gly Thr His Pro Leu Asn Pro Ala Asn Ser Ser His
 180 185 190
 Leu Leu Ser Leu Thr Leu Gly Pro Gln His Ala Asp Asn Ile Tyr Ile
 195 200 205
 Cys Thr Val Ser Asn Pro Ile Ser Asn Asn Ser Gln Thr Phe Ser Pro
 210 215 220
 Trp Pro Gly Cys Arg Thr Asp Pro Ser Glu Thr Lys Pro Trp Ala Val
 225 230 235 240
 Tyr Ala Gly Leu Leu Gly Gly Val Ile Met Ile Leu Ile Met Val Val
 245 250 255
 Ile Leu Gln Leu Arg Arg Arg Gly Lys Thr Asn His Tyr Gln Thr Thr
 260 265 270
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 Asp Thr His His Gln Thr Ser Asp Leu Phe
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<210> 288

<211> 3640

<212> DNA

<213> Homo sapiens

<400> 288

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<210> 289

<211> 628

<212> PRT

<213> Homo sapiens

<400> 289

Met	Gly	Ser	Cys	Ala	Arg	Leu	Leu	Leu	Trp	Gly	Cys	Thr	Val	Val	
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Ala	Ala	Gly	Leu	Ser	Gly	Val	Ala	Gly	Val	Ser	Ser	Arg	Cys	Glu	Lys
						20			25				30		
Ala	Cys	Asn	Pro	Arg	Met	Gly	Asn	Leu	Ala	Leu	Gly	Arg	Lys	Leu	Trp
					35				40			45			
Ala	Asp	Thr	Thr	Cys	Gly	Gln	Asn	Ala	Thr	Glu	Leu	Tyr	Cys	Phe	Tyr
					50				55			60			
Ser	Glu	Asn	Thr	Asp	Leu	Thr	Cys	Arg	Gln	Pro	Lys	Cys	Asp	Lys	Cys
	65				70				75			80			
Asn	Ala	Ala	Tyr	Pro	His	Leu	Ala	His	Leu	Pro	Ser	Ala	Met	Ala	Asp
					85				90			95			
Ser	Ser	Phe	Arg	Phe	Pro	Arg	Thr	Trp	Trp	Gln	Ser	Ala	Glu	Asp	Val
					100				105			110			
His	Arg	Glu	Lys	Ile	Gln	Leu	Asp	Leu	Glu	Ala	Glu	Phe	Tyr	Phe	Thr
					115				120			125			
His	Leu	Ile	Val	Met	Phe	Lys	Ser	Pro	Arg	Pro	Ala	Ala	Met	Val	Leu
					130				135			140			
Asp	Arg	Ser	Gln	Asp	Phe	Gly	Lys	Thr	Trp	Lys	Pro	Tyr	Lys	Tyr	Phe
	145				150				155			160			
Ala	Thr	Asn	Cys	Ser	Ala	Thr	Phe	Gly	Leu	Glu	Asp	Asp	Val	Val	Lys
					165				170			175			
Lys	Gly	Ala	Ile	Cys	Thr	Ser	Lys	Tyr	Ser	Ser	Pro	Phe	Pro	Cys	Thr
					180				185			190			
Gly	Gly	Glu	Val	Ile	Phe	Lys	Ala	Leu	Ser	Pro	Pro	Tyr	Asp	Thr	Glu
					195				200			205			
Asn	Pro	Tyr	Ser	Ala	Lys	Val	Gln	Gln	Leu	Lys	Ile	Thr	Asn	Leu	

210	215	220
Arg Val Gln Leu Leu Lys	Arg Gln Ser Cys	Pro Cys Gln Arg Asn Asp
225	230	235
Leu Asn Glu Glu Pro Gln His Phe Thr His Tyr Ala Ile Tyr Asp Phe		240
245	250	255
Ile Val Lys Gly Ser Cys Phe Cys Asn Gly His Ala Asp Gln Cys Ile		
260	265	270
Pro Val His Gly Phe Arg Pro Val Lys Ala Pro Gly Thr Phe His Met		
275	280	285
Val His Gly Lys Cys Met Cys Lys His Asn Thr Ala Gly Ser His Cys		
290	295	300
Gln His Cys Ala Pro Leu Tyr Asn Asp Arg Pro Trp Glu Ala Ala Asp		
305	310	315
Gly Lys Thr Gly Ala Pro Asn Glu Cys Arg Thr Cys Lys Cys Asn Gly		320
325	330	335
His Ala Asp Thr Cys His Phe Asp Val Asn Val Trp Glu Ala Ser Gly		
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Asn Arg Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn Thr Glu Gly		
355	360	365
Gln Tyr Cys Gln Arg Cys Lys Pro Gly Phe Tyr Arg Asp Leu Arg Arg		
370	375	380
Pro Phe Ser Ala Pro Asp Ala Cys Lys Pro Cys Ser Cys His Pro Val		
385	390	395
Gly Ser Ala Val Leu Pro Ala Asn Ser Val Thr Phe Cys Asp Pro Ser		400
405	410	415
Asn Gly Asp Cys Pro Cys Lys Pro Gly Val Ala Gly Arg Arg Cys Asp		
420	425	430
Arg Cys Met Val Gly Tyr Trp Gly Phe Gly Asp Tyr Gly Cys Arg Pro		
435	440	445
Cys Asp Cys Ala Gly Ser Cys Asp Pro Ile Thr Gly Asp Cys Ile Ser		
450	455	460
Ser His Thr Asp Ile Asp Trp Tyr His Glu Val Pro Asp Phe Arg Pro		
465	470	475
Val His Asn Lys Ser Glu Pro Ala Trp Glu Trp Glu Asp Ala Gln Gly		480
485	490	495
Phe Ser Ala Leu Leu His Ser Gly Lys Cys Glu Cys Lys Glu Gln Thr		
500	505	510
Leu Gly Asn Ala Lys Ala Phe Cys Gly Met Lys Tyr Ser Tyr Val Leu		
515	520	525
Lys Ile Lys Ile Leu Ser Ala His Asp Lys Gly Thr His Val Glu Val		
530	535	540
Asn Val Lys Ile Lys Lys Val Leu Lys Ser Thr Lys Leu Lys Ile Phe		
545	550	555
Arg Gly Lys Arg Thr Leu Tyr Pro Glu Ser Trp Thr Asp Arg Gly Cys		560
565	570	575
Thr Cys Pro Ile Leu Asn Pro Gly Leu Glu Tyr Leu Val Ala Gly His		
580	585	590
Glu Asp Ile Arg Thr Gly Lys Leu Ile Val Asn Met Lys Ser Phe Val		
595	600	605
Gln His Trp Lys Pro Ser Leu Gly Arg Lys Val Met Asp Ile Leu Lys		
610	615	620
Arg Glu Cys Lys		
625		

<210> 290
<211> 2540
<212> DNA
<213> Mouse

<400> 290

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gccacaccgc	ggaccccaga	ggaggcccag	cgtgtggaca	gcctgggtgg	gtcggggccg	240
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aaaaaaaaaaaa	aaaaaaaaaaa					2540

<210> 291
<211> 765
<212> PRT
<213> Mouse

<400> 291

Met	Leu	Leu	Arg	Leu	Leu	Leu	Ala	Trp	Val	Ala	Ala	Val	Pro	Ala	Leu
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				20			25		30						
Ser	Cys	Tyr	Ala	Leu	Phe	Pro	Arg	Arg	Arg	Thr	Phe	Leu	Glu	Ala	Trp
				35			40		45						
Arg	Ala	Cys	Arg	Glu	Leu	Gly	Gly	Asn	Leu	Ala	Thr	Pro	Arg	Thr	Pro
	50			55			60								
Glu	Glu	Ala	Gln	Arg	Val	Asp	Ser	Leu	Val	Gly	Val	Gly	Pro	Ala	Asn
65					70			75			80				
Gly	Leu	Leu	Trp	Ile	Gly	Leu	Gln	Arg	Gln	Ala	Arg	Gln	Cys	Gln	Pro
				85			90				95				

Gln Arg Pro Leu Arg Gly Phe Ile Trp Thr Thr Gly Asp Gln Asp Thr
 100 105 110
 Ala Phe Thr Asn Trp Ala Gln Pro Ala Thr Glu Gly Pro Cys Pro Ala
 115 120 125
 Gln Arg Cys Ala Ala Leu Glu Ala Ser Gly Glu His Arg Trp Leu Glu
 130 135 140
 Gly Ser Cys Thr Leu Ala Val Asp Gly Tyr Leu Cys Gln Phe Gly Phe
 145 150 155 160
 Glu Gly Ala Cys Pro Ala Leu Pro Leu Glu Val Gly Gln Ala Gly Pro
 165 170 175
 Ala Val Tyr Thr Thr Pro Phe Asn Leu Val Ser Ser Glu Phe Glu Trp
 180 185 190
 Leu Pro Phe Gly Ser Val Ala Ala Val Gln Cys Gln Ala Gly Arg Gly
 195 200 205
 Ala Ser Leu Leu Cys Val Lys Gln Pro Ser Gly Gly Val Gly Trp Ser
 210 215 220
 Gln Thr Gly Pro Leu Cys Pro Gly Thr Gly Cys Gly Pro Asp Asn Gly
 225 230 235 240
 Gly Cys Glu His Glu Cys Val Glu Glu Val Asp Gly Ala Val Ser Cys
 245 250 255
 Arg Cys Ser Glu Gly Phe Arg Leu Ala Ala Asp Gly His Ser Cys Glu
 260 265 270
 Asp Pro Cys Ala Gln Ala Pro Cys Glu Gln Cys Glu Pro Gly Gly
 275 280 285
 Pro Gln Gly Tyr Ser Cys His Cys Arg Leu Gly Phe Arg Pro Ala Glu
 290 295 300
 Asp Asp Pro His Arg Cys Val Asp Thr Asp Glu Cys Gln Ile Ala Gly
 305 310 315 320
 Val Cys Gln Gln Met Cys Val Asn Tyr Val Gly Gly Phe Glu Cys Tyr
 325 330 335
 Cys Ser Glu Gly His Glu Leu Glu Ala Asp Gly Ile Ser Cys Ser Pro
 340 345 350
 Ala Gly Ala Met Gly Ala Gln Ala Ser Gln Asp Leu Arg Asp Glu Leu
 355 360 365
 Leu Asp Asp Gly Glu Glu Gly Glu Asp Glu Glu Glu Pro Trp Glu Asp
 370 375 380
 Phe Asp Gly Thr Trp Thr Glu Glu Gln Gly Ile Leu Trp Leu Ala Pro
 385 390 395 400
 Thr His Pro Pro Asp Phe Gly Leu Pro Tyr Arg Pro Asn Phe Pro Gln
 405 410 415
 Asp Gly Glu Pro Gln Arg Leu His Leu Glu Pro Thr Trp Pro Pro Pro
 420 425 430
 Leu Ser Ala Pro Arg Gly Pro Tyr His Ser Ser Val Val Ser Ala Thr
 435 440 445
 Arg Pro Met Val Ile Ser Ala Thr Arg Pro Thr Leu Pro Ser Ala His
 450 455 460
 Lys Thr Ser Val Ile Ser Ala Thr Arg Pro Pro Leu Ser Pro Val His
 465 470 475 480
 Pro Pro Ala Met Ala Pro Ala Thr Pro Pro Ala Val Phe Ser Glu His
 485 490 495
 Gln Ile Pro Lys Ile Lys Ala Asn Tyr Pro Asp Leu Pro Phe Gly His
 500 505 510
 Lys Pro Gly Ile Thr Ser Ala Thr His Pro Ala Arg Ser Pro Pro Tyr
 515 520 525
 Gln Pro Pro Ile Ile Ser Thr Asn Tyr Pro Gln Val Phe Pro Pro His
 530 535 540
 Gln Ala Pro Met Ser Pro Asp Thr His Thr Ile Thr Tyr Leu Pro Pro
 545 550 555 560
 Val Pro Pro His Leu Asp Pro Gly Asp Thr Thr Ser Lys Ala His Gln
 565 570 575
 His Pro Leu Leu Pro Asp Ala Pro Gly Ile Arg Thr Gln Ala Pro Gln

	580	585	590
Leu Ser Val Ser Ala Leu Gln Pro Pro Leu Pro Thr Asn Ser Arg Ser			
595	600	605	
Ser Val His Glu Thr Pro Val Pro Ala Ala Asn Gln Pro Pro Ala Phe			
610	615	620	
Pro Ser Ser Pro Leu Pro Pro Gln Arg Pro Thr Asn Gln Thr Ser Ser			
625	630	635	640
Ile Ser Pro Thr His Ser Tyr Ser Arg Ala Pro Leu Val Pro Arg Glu			
645	650	655	
Gly Val Pro Ser Pro Lys Ser Val Pro Gln Leu Pro Ser Val Pro Ser			
660	665	670	
Thr Ala Ala Pro Thr Ala Leu Ala Glu Ser Gly Leu Ala Gly Gln Ser			
675	680	685	
Gln Arg Asp Asp Arg Trp Leu Leu Val Ala Leu Leu Val Pro Thr Cys			
690	695	700	
Val Phe Leu Val Val Leu Leu Ala Leu Gly Ile Val Tyr Cys Thr Arg			
705	710	715	720
Cys Gly Ser His Ala Pro Asn Lys Arg Ile Thr Asp Cys Tyr Arg Trp			
725	730	735	
Val Thr His Ala Gly Asn Lys Ser Ser Thr Glu Pro Met Pro Pro Arg			
740	745	750	
Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr Ser Val			
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<210> 292

<211> 3020

<212> DNA

<213> Mouse

<400> 292

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gctgggagca	gccgggtggc	tcatgactac	tcagagagtc	tgcccaaaga	aaagagtctt	300
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<210> 293
<211> 266
<212> PRT
<213> Mouse

<400> 293

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35 40 45	
Thr Pro Thr Ile Glu Asp Phe His Arg Lys Val Tyr Asn Ile His Gly	
50 55 60	
Asp Met Tyr Gln Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe	
65 70 75 80	
Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu	
85 90 95	
Val Phe Ser Leu Asp Ser Arg Glu Ser Phe Asp Glu Val Lys Arg Leu	
100 105 110	
Gln Lys Gln Ile Leu Glu Val Lys Ser Cys Leu Lys Asn Lys Thr Lys	
115 120 125	
Glu Ala Ala Glu Leu Pro Met Val Ile Cys Gly Asn Lys Asn Asp His	
130 135 140	
Ser Glu Leu Cys Arg Gln Val Pro Ala Met Glu Ala Glu Leu Leu Val	
145 150 155 160	
Ser Gly Asp Glu Asn Cys Ala Tyr Phe Glu Val Ser Ala Lys Lys Asn	
165 170 175	
Thr Asn Val Asn Glu Met Phe Tyr Val Leu Phe Ser Met Ala Lys Leu	
180 185 190	
Pro His Glu Met Ser Pro Ala Leu His His Lys Ile Ser Val Gln Tyr	
195 200 205	
Gly Asp Ala Phe His Pro Arg Pro Phe Cys Met Arg Arg Thr Lys Val	
210 215 220	
Ala Gly Ala Tyr Gly Met Val Ser Pro Phe Ala Arg Arg Pro Ser Val	
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260 265	

<210> 294
<211> 5520
<212> DNA
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<400> 294

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<210> 295

<211> 1329

<212> PRT

<213> Mouse

<400> 295

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Leu	Leu	Leu	Leu	Ala	Pro	Gly	Thr	Arg	Gly	Ala	Pro	Gly	Cys	Pro	Val
							20		25				30		
Pro	Ile	Arg	Gly	Cys	Lys	Cys	Ser	Gly	Glu	Arg	Pro	Lys	Gly	Leu	Ser
							35		40			45			
Gly	Gly	Ala	His	Asn	Pro	Ala	Arg	Arg	Arg	Val	Val	Cys	Gly	Gly	Gly
							50		55			60			
Asp	Leu	Pro	Glu	Pro	Pro	Asp	Pro	Gly	Leu	Leu	Pro	Asn	Gly	Thr	Ile
							65		70			75			80
Thr	Leu	Leu	Leu	Ser	Asn	Asn	Lys	Ile	Thr	Gly	Leu	Arg	Asn	Gly	Ser
							85		90			95			
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Glu	Lys	Leu	Asp	Leu	Arg	Ser	Asn	Val

	100	105	110
Ile Ser Thr Val Gln Pro Gly Ala Phe Leu Gly Leu Gly Glu Leu Lys			
115	120	125	
Arg Leu Asp Leu Ser Asn Asn Arg Ile Gly Cys Leu Thr Ser Glu Thr			
130	135	140	
Phe Gln Gly Leu Pro Arg Leu Leu Arg Leu Asn Ile Ser Gly Asn Ile			
145	150	155	160
Tyr Ser Ser Leu Gln Pro Gly Val Phe Asp Glu Leu Pro Ala Leu Lys			
165	170	175	
Ile Val Asp Phe Gly Thr Glu Phe Leu Thr Cys Asp Cys Arg Leu Arg			
180	185	190	
Trp Leu Leu Pro Trp Ala Arg Asn His Ser Leu Gln Leu Ser Glu Arg			
195	200	205	
Thr Leu Cys Ala Tyr Pro Ser Ala Leu His Ala His Ala Leu Ser Ser			
210	215	220	
Leu Gln Glu Ser Gln Leu Arg Cys Glu Gly Ala Leu Glu Leu His Thr			
225	230	235	240
His Tyr Leu Ile Pro Ser Leu Arg Gln Val Val Phe Gln Gly Asp Arg			
245	250	255	
Leu Pro Phe Gln Cys Ser Ala Ser Tyr Leu Gly Asn Asp Thr Arg Ile			
260	265	270	
His Trp Tyr His Asn Gly Ala Pro Met Glu Ser Asp Glu Gln Ala Gly			
275	280	285	
Ile Val Leu Ala Glu Asn Leu Ile His Asp Cys Thr Phe Ile Thr Ser			
290	295	300	
Glu Leu Thr Leu Ser His Ile Gly Val Trp Ala Ser Gly Glu Trp Glu			
305	310	315	320
Cys Ser Val Ser Thr Val Gln Gly Asn Thr Ser Lys Lys Val Glu Ile			
325	330	335	
Val Val Leu Glu Thr Ser Ala Ser Tyr Cys Pro Ala Glu Arg Val Thr			
340	345	350	
Asn Asn Arg Gly Asp Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr			
355	360	365	
Ala Tyr Gln Ser Cys Leu Gln Tyr Pro Phe Thr Ser Val Pro Leu Ser			
370	375	380	
Gly Gly Ala Pro Gly Thr Arg Ala Ser Arg Arg Cys Asp Arg Ala Gly			
385	390	395	400
Arg Trp Glu Pro Gly Asp Tyr Ser His Cys Leu Tyr Thr Asn Asp Ile			
405	410	415	
Thr Arg Val Leu Tyr Thr Phe Val Leu Met Pro Ile Asn Ala Ser Asn			
420	425	430	
Ala Leu Thr Leu Ala His Gln Leu Arg Val Tyr Thr Ala Glu Ala Ala			
435	440	445	
Ser Phe Ser Asp Met Met Asp Val Val Tyr Val Ala Gln Met Ile Gln			
450	455	460	
Lys Phe Leu Gly Tyr Val Asp Gln Ile Lys Glu Leu Val Glu Val Met			
465	470	475	480
Val Asp Met Ala Ser Asn Leu Met Leu Val Asp Glu His Leu Leu Trp			
485	490	495	
Leu Ala Gln Arg Glu Asp Lys Ala Cys Ser Gly Ile Val Gly Ala Leu			
500	505	510	
Glu Arg Ile Gly Gly Ala Ala Leu Ser Pro His Ala Gln His Ile Ser			
515	520	525	
Val Asn Ser Arg Asn Val Ala Leu Glu Ala Tyr Leu Ile Lys Pro His			
530	535	540	
Ser Tyr Val Gly Leu Thr Cys Thr Ala Phe Gln Arg Arg Glu Val Gly			
545	550	555	560
Val Ser Gly Ala Gln Pro Ser Ser Val Gly Gln Asp Ala Pro Val Glu			
565	570	575	
Pro Glu Pro Leu Ala Asp Gln Gln Leu Arg Phe Arg Cys Thr Thr Gly			
580	585	590	

Arg Pro Asn Ile Ser Leu Ser Ser Phe His Ile Lys Asn Ser Val Ala
 595 600 605
 Leu Ala Ser Ile Gln Leu Pro Pro Ser Leu Phe Ser Thr Leu Pro Ala
 610 615 620
 Ala Leu Ala Pro Pro Val Pro Pro Asp Cys Thr Leu Gln Leu Leu Val
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 Phe Arg Asn Gly Arg Leu Phe Arg Ser His Gly Asn Asn Thr Ser Arg
 645 650 655
 Pro Gly Ala Ala Gly Pro Gly Lys Arg Arg Gly Val Ala Thr Pro Val
 660 665 670
 Ile Phe Ala Gly Thr Ser Gly Cys Gly Val Gly Asn Leu Thr Glu Pro
 675 680 685
 Val Ala Val Ser Leu Arg His Trp Ala Glu Gly Ala Asp Pro Met Ala
 690 695 700
 Ala Trp Trp Asn Gln Asp Gly Pro Gly Gly Trp Ser Ser Glu Gly Cys
 705 710 715 720
 Arg Leu Arg Tyr Ser Gln Pro Asn Val Ser Ser Leu Tyr Cys Gln His
 725 730 735
 Leu Gly Asn Val Ala Val Leu Met Glu Leu Asn Ala Phe Pro Arg Glu
 740 745 750
 Ala Gly Gly Ser Gly Ala Gly Leu His Pro Val Val Tyr Pro Cys Thr
 755 760 765
 Ala Leu Leu Leu Cys Leu Phe Ser Thr Ile Ile Thr Tyr Ile Leu
 770 775 780
 Asn His Ser Ser Ile His Val Ser Arg Lys Gly Trp His Met Leu Leu
 785 790 795 800
 Asn Leu Cys Phe His Met Ala Met Thr Ser Ala Val Phe Val Gly Gly
 805 810 815
 Val Thr Leu Thr Asn Tyr Gln Met Val Cys Gln Ala Val Gly Ile Thr
 820 825 830
 Leu His Tyr Ser Ser Leu Ser Ser Leu Leu Trp Met Gly Val Lys Ala
 835 840 845
 Arg Val Leu His Lys Glu Leu Ser Trp Arg Ala Pro Pro Leu Glu Glu
 850 855 860
 Gly Glu Ala Ala Pro Pro Gly Pro Arg Pro Met Leu Arg Phe Tyr Leu
 865 870 875 880
 Ile Ala Gly Gly Ile Pro Leu Ile Ile Cys Gly Ile Thr Ala Ala Val
 885 890 895
 Asn Ile His Asn Tyr Arg Asp His Ser Pro Tyr Cys Trp Leu Val Trp
 900 905 910
 Arg Pro Ser Leu Gly Ala Phe Tyr Ile Pro Val Ala Leu Ile Leu Pro
 915 920 925
 Ile Thr Trp Ile Tyr Phe Leu Cys Ala Gly Leu His Leu Arg Ser His
 930 935 940
 Val Ala Gln Asn Pro Lys Gln Gly Asn Arg Ile Ser Leu Glu Pro Gly
 945 950 955 960
 Glu Glu Leu Arg Gly Ser Thr Arg Leu Arg Ser Ser Gly Val Leu Leu
 965 970 975
 Asn Asp Ser Gly Ser Leu Leu Ala Thr Val Ser Ala Gly Val Gly Thr
 980 985 990
 Pro Ala Pro Pro Glu Asp Gly Asp Gly Val Tyr Ser Pro Gly Val Gln
 995 1000 1005
 Leu Gly Ala Leu Met Thr Thr His Phe Leu Tyr Leu Ala Met Trp Ala
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 Cys Gly Ala Leu Ala Val Ser Gln Arg Trp Leu Pro Arg Val Val Cys
 1025 1030 1035 1040
 Ser Cys Leu Tyr Gly Val Ala Ala Ser Ala Leu Gly Leu Phe Val Phe
 1045 1050 1055
 Thr His His Cys Ala Arg Arg Arg Asp Val Arg Ala Ser Trp Arg Ala
 1060 1065 1070
 Cys Cys Pro Pro Ala Ser Pro Ser Ala Ser His Val Pro Ala Arg Ala

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Leu Pro Thr Ala Thr Glu Asp Gly Ser Pro Val	Leu Gly Glu Gly Pro	
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Ala Ser Leu Lys Ser Ser Pro Ser Gly Ser Ser	Gly Arg Ala Pro Pro	
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Pro Pro Cys Lys Leu Thr Asn Leu Gln Val Ala Gln Ser Gln Val Cys		
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Glu Ala Ser Val Ala Ala Arg Gly Asp Gly Glu Pro Glu Pro Thr Gly		
1140 1145	1150	
Ser Arg Gly Ser Leu Ala Pro Arg His His Asn Asn Leu His His Gly		
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Arg Arg Val His Lys Ser Arg Ala Lys Gly His Arg Ala Gly Glu Thr		
1170 1175	1180	
Gly Gly Lys Ser Arg Leu Lys Ala Leu Arg Ala Gly Thr Ser Pro Gly		
1185 1190	1195 1200	
Ala Pro Glu Leu Leu Ser Ser Glu Ser Gly Ser Leu His Asn Ser Pro		
1205 1210	1215	
Ser Asp Ser Tyr Pro Gly Ser Ser Arg Asn Ser Pro Gly Asp Gly Leu		
1220 1225	1230	
Pro Leu Glu Gly Glu Pro Met Leu Thr Pro Ser Glu Gly Ser Asp Thr		
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Ser Ala Ala Pro Ile Ala Glu Thr Gly Arg Pro Gly Gln Arg Arg Ser		
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Ala Ser Arg Asp Asn Leu Lys Gly Ser Gly Ser Ala Leu Glu Arg Glu		
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Ser Lys Arg Arg Ser Tyr Pro Leu Asn Thr Thr Ser Leu Asn Gly Ala		
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Pro Lys Gly Gly Lys Tyr Glu Asp Ala Ser Val Thr Gly Ala Glu Ala		
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<210> 296
 <211> 2840
 <212> DNA
 <213> Mouse

<400> 296

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<210> 297

<211> 500

<212> PRT

<213> Mouse

<400> 297

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Asp Ser Ala Trp Thr Ala Lys Arg Thr Arg Gln Gly Trp Ser Arg Arg	
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Ser Gln Asp Leu Gly Gly Ser Leu Ala Ile Asp Thr Leu Pro Asp	
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Asn Arg Thr Arg Val Val Glu Asp Asn His Asn Tyr Tyr Val Ser Arg	
85 90 95	
Val Tyr Gly Pro Gly Glu Lys Gln Ser Gln Asp Leu Trp Val Asp Leu	
100 105 110	
Ala Val Ala Asn Arg Ser His Val Lys Ile His Arg Ile Leu Ser Ser	
115 120 125	
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130 135 140	
Tyr Gly His Pro Leu Arg Gln Ile Thr Ile Ala Thr Gly Gly Phe Ile	
145 150 155 160	
Phe Met Gly Asp Met Leu His Arg Met Leu Thr Ala Thr Gln Tyr Val	
165 170 175	
Ala Pro Leu Met Ala Asn Phe Asn Pro Gly Tyr Ser Asp Asn Ser Thr	
180 185 190	
Val Ala Tyr Phe Asp Asn Gly Thr Val Phe Val Val Gln Trp Asp His	
195 200 205	
Val Tyr Leu Gln Asp Arg Glu Asp Arg Gly Ser Phe Thr Phe Gln Ala	

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Ala Leu His Arg Asp Gly Arg Ile Val Phe Gly Tyr Lys Glu Ile Pro		
225	230	235
Met Ala Val Leu Asp Ile Ser Ser Ala Gln His Pro Val Lys Ala Gly		240
245	250	255
Leu Ser Asp Ala Phe Met Ile Leu Asn Ser Ser Pro Glu Val Pro Glu		
260	265	270
Ser Gln Arg Arg Thr Ile Phe Glu Tyr His Arg Val Glu Leu Asp Ser		
275	280	285
Ser Lys Ile Thr Thr Ser Ala Val Glu Phe Thr Pro Leu Pro Thr		
290	295	300
Cys Leu Gln His Gln Ser Cys Asp Thr Cys Val Ser Ser Asn Leu Thr		
305	310	315
Phe Asn Cys Ser Trp Cys His Val Leu Gln Arg Cys Ser Ser Gly Phe		320
325	330	335
Asp Arg Tyr Arg Gln Glu Trp Leu Thr Tyr Gly Cys Ala Gln Glu Ala		
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Glu Gly Lys Thr Cys Glu Asp Phe Gln Asp Asp Ser His Tyr Ser Ala		
355	360	365
Ser Pro Asp Ser Ser Phe Ser Pro Phe Asn Gly Asp Ser Thr Thr Ser		
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Ser Ser Leu Phe Ile Asp Ser Leu Thr Thr Glu Asp Asp Thr Lys Leu		
385	390	395
Asn Pro Tyr Ala Glu Gly Asp Gly Leu Pro Asp His Ser Ser Pro Lys		
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Ser Lys Gly Pro Pro Val His Leu Gly Thr Ile Val Gly Ile Val Leu		
420	425	430
Ala Val Leu Leu Val Ala Ala Ile Ile Leu Ala Gly Ile Tyr Ile Ser		
435	440	445
Gly His Pro Asn Ser Asn Ala Ala Leu Phe Phe Ile Glu Arg Arg Pro		
450	455	460
His His Trp Pro Ala Met Lys Phe His Asn His Pro Asn His Ser Thr		
465	470	475
Tyr Thr Glu Val Glu Pro Ser Gly His Glu Lys Glu Gly Phe Val Glu		480
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Ala Glu Gln Cys		
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<210> 298
 <211> 2010
 <212> DNA
 <213> Mouse

<400> 298

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<210> 299

<211> 530

<212> PRT

<213> Mouse

<400> 299

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Leu	Cys	His	Phe	Leu	Thr	Asp	Arg	Phe	His	Phe	Ala	His	Gly	Glu	Pro
									20			25		30	
Gly	His	His	Thr	Asn	Asp	Trp	Ile	Tyr	Glu	Val	Thr	Asn	Ala	Phe	Pro
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Trp	Asn	Glu	Glu	Gly	Val	Glu	Val	Asp	Ser	Gln	Ala	Tyr	Asn	His	Arg
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Trp	Lys	Arg	Asn	Val	Asp	Pro	Phe	Lys	Ala	Val	Asp	Thr	Asn	Arg	Ala
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Ser	Met	Gly	Gln	Ala	Ser	Pro	Glu	Ser	Lys	Gly	Phe	Thr	Asp	Leu	Leu
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Leu	Asp	Asp	Gly	Gln	Asp	Asn	Asn	Thr	Gln	Ile	Glu	Asp	Thr	Asp	
							100		105			110			
His	Asn	Tyr	Tyr	Ile	Ser	Arg	Ile	Tyr	Gly	Pro	Ala	Asp	Ser	Ala	Ser
						115			120			125			
Arg	Asp	Leu	Trp	Val	Asn	Ile	Asp	Gln	Met	Glu	Lys	Asp	Lys	Val	Lys
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Ile	His	Gly	Ile	Leu	Ser	Asn	Thr	His	Arg	Gln	Ala	Ala	Arg	Val	Asn
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Leu	Ser	Phe	Asp	Phe	Pro	Phe	Tyr	Gly	His	Phe	Leu	Asn	Glu	Val	Thr
							165			170			175		
Val	Ala	Thr	Gly	Gly	Phe	Ile	Tyr	Thr	Gly	Glu	Val	Val	His	Arg	Met
						180			185			190			
Leu	Thr	Ala	Thr	Gln	Tyr	Ile	Ala	Pro	Leu	Met	Ala	Asn	Phe	Asp	Pro
						195			200			205			
Ser	Val	Ser	Arg	Asn	Ser	Thr	Val	Arg	Tyr	Phe	Asp	Asn	Gly	Thr	Ala
						210			215			220			
Leu	Val	Val	Gln	Trp	Asp	His	Val	His	Leu	Gln	Asp	Asn	Tyr	Asn	Leu
							225		230			235			240
Gly	Ser	Phe	Thr	Phe	Gln	Ala	Thr	Leu	Leu	Met	Asp	Gly	Arg	Ile	Ile
							245			250			255		
Phe	Gly	Tyr	Lys	Glu	Ile	Pro	Val	Leu	Val	Thr	Gln	Ile	Ser	Ser	Thr
							260			265			270		
Asn	His	Pro	Val	Lys	Val	Gly	Leu	Ser	Asp	Ala	Phe	Val	Val	Val	His
							275			280			285		
Arg	Ile	Gln	Gln	Ile	Pro	Asn	Val	Arg	Arg	Arg	Thr	Ile	Tyr	Glu	Tyr

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Glu Met Thr Pro Leu Pro Thr Cys Leu Gln Phe Asn Gly Cys Gly Pro		320
325	330	335
Cys Val Ser Ser Gln Ile Gly Phe Asn Cys Ser Trp Cys Ser Lys Leu		
340	345	350
Gln Arg Cys Ser Ser Gly Phe Asp Arg His Arg Gln Asp Trp Val Asp		
355	360	365
Ser Gly Cys Pro Glu Glu Val Gln Ser Lys Glu Lys Met Cys Glu Lys		
370	375	380
Thr Glu Pro Gly Glu Thr Ser Gln Thr Thr Thr Ser His Thr Thr		
385	390	395
400		
Thr Met Gln Phe Arg Val Leu Thr Thr Arg Arg Ala Val Thr Ser		
405	410	415
Gln Met Pro Thr Ser Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu		
420	425	430
His Leu Lys Asp Ser Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys		
435	440	445
Lys Gly Gly Thr Leu His Ala Gly Leu Ile Val Gly Ile Leu Ile Leu		
450	455	460
Val Leu Ile Ile Ala Ala Ile Leu Val Thr Val Tyr Met Tyr His		
465	470	475
480		
His Pro Thr Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser		
485	490	495
Arg Trp Pro Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala Tyr		
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515	520	525
Gln Cys		
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<210> 300
 <211> 5220
 <212> DNA
 <213> Mouse

<400> 300

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<210> 301
 <211> 562
 <212> PRT
 <213> Mouse

<400> 301
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 Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp
 35 40 45
 Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val
 50 55 60
 Glu Gln Leu Ala His Arg Phe Ile Ser Pro Gln Leu Arg Met Ser Phe
 65 70 75 80
 Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp
 85 90 95
 Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro
 100 105 110
 Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln
 115 120 125
 Ile Tyr Tyr Glu Asn Ser Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile
 130 135 140
 Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu
 145 150 155 160
 Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val
 165 170 175
 Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser
 180 185 190
 Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly
 195 200 205
 Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala
 210 215 220
 Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg
 225 230 235 240
 Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser
 245 250 255
 Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ala Val
 260 265 270
 Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly
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 Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile
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 Ser Ser Ser Val Ile Ile Thr Thr His Cys Ser Asp Gly Ser Ile
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 325 330 335
 Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys Glu Val
 340 345 350
 Pro Pro Pro Pro Val Glu Glu Ser Glu Glu Glu Asp Asp Asp Gly Leu
 355 360 365
 Pro Lys Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly Gly Arg
 370 375 380

Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu Lys Gly
 385 390 395 400
 Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Asn Ala Arg Val
 405 410 415
 Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn Leu Asn
 420 425 430
 Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser Pro Ile
 435 440 445
 Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly Tyr Asp
 450 455 460
 Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg Cys Ile
 465 470 475 480
 Asn Phe Thr Arg Val Lys Asn Ser Gln Pro Ala Lys Tyr Pro Leu Asn
 485 490 495
 Asn Thr Tyr His Pro Ser Ser Pro Pro Ala Pro Ile Tyr Thr Pro
 500 505 510
 Pro Pro Pro Ala Pro His Cys Pro Pro Pro Ala Pro Ser Ala Pro Thr
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 Ser Val

<210> 302
 <211> 2690
 <212> DNA
 <213> Mouse

<400> 302

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<210> 303

<211> 162

<212> PRT

<213> Mouse

<400> 303

Met	Asn	Pro	Ala	Ile	Ser	Val	Ala	Leu	Leu	Leu	Ser	Val	Leu	Gln	Val
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Ser	Arg	Gly	Gln	Lys	Val	Thr	Ser	Leu	Thr	Ala	Cys	Leu	Val	Asn	Gln
				20				25			30				
Asn	Leu	Arg	Leu	Asp	Cys	Arg	His	Glu	Asn	Asn	Thr	Lys	Asp	Asn	Ser
				35				40			45				
Ile	Gln	His	Glu	Phe	Ser	Leu	Thr	Arg	Glu	Lys	Arg	Lys	His	Val	Leu
				50				55			60				
Ser	Gly	Thr	Leu	Gly	Ile	Pro	Glu	His	Thr	Tyr	Arg	Ser	Arg	Val	Thr
				65				70			75			80	
Leu	Ser	Asn	Gln	Pro	Tyr	Ile	Lys	Val	Leu	Thr	Leu	Ala	Asn	Phe	Thr
				85				90			95				
Thr	Lys	Asp	Glu	Gly	Asp	Tyr	Phe	Cys	Glu	Leu	Gln	Val	Ser	Gly	Ala
				100				105			110				
Asn	Pro	Met	Ser	Ser	Asn	Lys	Ser	Ile	Ser	Val	Tyr	Arg	Asp	Lys	Leu
				115				120			125				
Val	Lys	Cys	Gly	Gly	Ile	Ser	Leu	Leu	Val	Gln	Asn	Thr	Ser	Trp	Met
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Leu	Leu	Leu	Leu	Ser	Leu	Ser	Leu	Leu	Gln	Ala	Leu	Asp	Phe	Ile	
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Ser	Leu														

<210> 304

<211> 4588

<212> DNA

<213> Mouse

<400> 304

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<210> 305
<211> 1479
<212> PRT
<213> Mouse

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Ser Ala Ala Ala Leu Leu Glu Pro Asp Val Phe Leu Ile Phe Ser Gln	
35 40 45	
Gly Met Gln Gly Cys Leu Glu Ala Gln Gly Val Gln Val Arg Val Thr	
50 55 60	
Pro Phe Cys Asn Ala Ser Leu Pro Ala Gln Arg Trp Lys Trp Val Ser	
65 70 75 80	
Arg Asn Arg Leu Phe Asn Leu Gly Ala Thr Gln Cys Leu Gly Thr Gly	
85 90 95	
Trp Pro Val Thr Asn Thr Thr Val Ser Leu Gly Met Tyr Glu Cys Asp	
100 105 110	
Arg Glu Ala Leu Ser Leu Arg Met Ala Val Ser Tyr Thr Arg Gly Pro	
115 120 125	
Val Val Pro Ala Ser Gly Gly Ser Cys Lys Gln Cys Ile Gln Ala Trp	
130 135 140	
His Leu Glu Arg Gly Asp Gln Thr Arg Ser Gly His Trp Asn Ile Tyr	
145 150 155 160	
Gly Ser Glu Glu Asp Leu Cys Ala Arg Pro Tyr Tyr Glu Val Tyr Thr	
165 170 175	
Ile Gln Gly Asn Ser His Gly Lys Pro Cys Thr Ile Pro Phe Lys Tyr	
180 185 190	
Asp Asn Gln Trp Phe His Gly Cys Thr Ser Thr Gly Arg Glu Asp Gly	
195 200 205	
His Leu Trp Cys Ala Thr Thr Gln Asp Tyr Gly Lys Asp Glu Arg Trp	
210 215 220	
Gly Phe Cys Pro Ile Lys Ser Asn Asp Cys Glu Thr Phe Trp Asp Lys	
225 230 235 240	
Asp Gln Leu Thr Asp Ser Cys Tyr Gln Phe Asn Phe Gln Ser Thr Leu	
245 250 255	
Ser Trp Arg Glu Ala Trp Ala Ser Cys Glu Gln Gln Gly Ala Asp Leu	
260 265 270	
Leu Ser Ile Thr Glu Ile His Glu Gln Thr Tyr Ile Asn Gly Leu Leu	
275 280 285	
Thr Gly Tyr Ser Ser Thr Leu Trp Ile Gly Leu Asn Asp Leu Asp Thr	
290 295 300	
Ser Gly Gly Trp Gln Trp Ser Asp Asn Ser Pro Leu Lys Tyr Leu Asn	
305 310 315 320	
Trp Glu Ser Asp Gln Pro Asp Asn Pro Gly Glu Glu Asn Cys Gly Val	
325 330 335	
Ile Arg Thr Glu Ser Ser Gly Gly Trp Gln Asn His Asp Cys Ser Ile	
340 345 350	
Ala Leu Pro Tyr Val Cys Lys Lys Pro Asn Ala Thr Val Glu Pro	
355 360 365	
Ile Gln Pro Asp Arg Trp Thr Asn Val Lys Val Glu Cys Asp Pro Ser	
370 375 380	

Trp Gln Pro Phe Gln Gly His Cys Tyr Arg Leu Gln Ala Glu Lys Arg
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 Ser Trp Gln Glu Ser Lys Arg Ala Cys Leu Arg Gly Gly Asp Leu
 405 410 415
 Leu Ser Ile His Ser Met Ala Glu Leu Glu Phe Ile Thr Lys Gln Ile
 420 425 430
 Lys Gln Glu Val Glu Glu Leu Trp Ile Gly Leu Asn Asp Leu Lys Leu
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 Gln Met Asn Phe Glu Trp Ser Asp Gly Ser Leu Val Ser Phe Thr His
 450 455 460
 Trp His Pro Phe Glu Pro Asn Asn Phe Arg Asp Ser Leu Glu Asp Cys
 465 470 475 480
 Val Thr Ile Trp Gly Pro Glu Gly Arg Trp Asn Asp Ser Pro Cys Asn
 485 490 495
 Gln Ser Leu Pro Ser Ile Cys Lys Lys Ala Gly Arg Leu Ser Gln Gly
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 Ala Ala Glu Glu Asp His Asp Cys Arg Lys Gly Trp Thr Trp His Ser
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 Pro Ser Cys Tyr Trp Leu Gly Glu Asp Gln Val Ile Tyr Ser Asp Ala
 530 535 540
 Arg Arg Leu Cys Thr Asp His Gly Ser Gln Leu Val Thr Ile Thr Asn
 545 550 555 560
 Arg Phe Glu Gln Ala Phe Val Ser Ser Leu Ile Tyr Asn Trp Glu Gly
 565 570 575
 Glu Tyr Phe Trp Thr Ala Leu Gln Asp Leu Asn Ser Thr Gly Ser Phe
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 Arg Trp Leu Ser Gly Asp Glu Val Ile Tyr Thr His Trp Asn Arg Asp
 595 600 605
 Gln Pro Gly Tyr Arg Arg Gly Gly Cys Val Ala Leu Ala Thr Gly Ser
 610 615 620
 Ala Met Gly Leu Trp Glu Val Lys Asn Cys Thr Ser Phe Arg Ala Arg
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 645 650 655
 Gly Pro Asp Pro Thr Pro Ser Leu Thr Gly Ser Cys Pro Gln Gly Trp
 660 665 670
 Val Ser Asp Pro Lys Leu Arg His Cys Tyr Lys Val Phe Ser Ser Glu
 675 680 685
 Arg Leu Gln Glu Lys Lys Ser Trp Ile Gln Ala Leu Gly Val Cys Arg
 690 695 700
 Glu Leu Gly Ala Gln Leu Leu Ser Leu Ala Ser Tyr Glu Glu Glu His
 705 710 715 720
 Phe Val Ala His Met Leu Asn Lys Ile Phe Gly Glu Ser Glu Pro Glu
 725 730 735
 Ser His Glu Gln His Trp Phe Trp Ile Gly Leu Asn Arg Arg Asp Pro
 740 745 750
 Arg Glu Gly His Ser Trp Arg Trp Ser Asp Gly Leu Gly Phe Ser Tyr
 755 760 765
 His Asn Phe Ala Arg Ser Arg His Asp Asp Asp Asp Ile Arg Gly Cys
 770 775 780
 Ala Val Leu Asp Leu Ala Ser Leu Gln Trp Val Pro Met Gln Cys Gln
 785 790 795 800
 Thr Gln Leu Asp Trp Ile Cys Lys Ile Pro Arg Gly Val Asp Val Arg
 805 810 815
 Glu Pro Asp Ile Gly Arg Gln Gly Arg Leu Glu Trp Val Arg Phe Gln
 820 825 830
 Glu Ala Glu Tyr Lys Phe Phe Glu His His Ser Ser Trp Ala Gln Ala
 835 840 845
 Gln Arg Ile Cys Thr Trp Phe Gln Ala Asp Leu Thr Ser Val His Ser
 850 855 860
 Gln Ala Glu Leu Gly Phe Leu Gly Gln Asn Leu Gln Lys Leu Ser Ser

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Gly Arg Phe Arg Trp Thr Asp Gly Ser Ile Ile Asn Phe Ile Ser Trp			
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Ala Pro Gly Lys Pro Arg Pro Ile Gly Lys Asp Lys Lys Cys Val Tyr			
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Met Thr Ala Arg Gln Glu Asp Trp Gly Asp Gln Arg Cys His Thr Ala			
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Leu Pro Tyr Ile Cys Lys Arg Ser Asn Ser Ser Gly Glu Thr Gln Pro			
945	950	955	960
Gln Asp Leu Pro Pro Ser Ala Leu Gly Gly Cys Pro Ser Gly Trp Asn			
965	970	975	
Gln Phe Leu Asn Lys Cys Phe Arg Ile Gln Gly Gln Asp Pro Gln Asp			
980	985	990	
Arg Val Lys Trp Ser Glu Ala Gln Phe Ser Cys Glu Gln Glu Ala			
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Gln Leu Val Thr Ile Ala Asn Pro Leu Glu Gln Ala Phe Ile Thr Ala			
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Ser Leu Pro Asn Val Thr Phe Asp Leu Trp Ile Gly Leu His Ala Ser			
1025	1030	1035	1040
Gln Arg Asp Phe Gln Trp Ile Glu Gln Glu Pro Leu Leu Tyr Thr Asn			
1045	1050	1055	
Trp Ala Pro Gly Glu Pro Ser Gly Pro Ser Pro Ala Pro Ser Gly Thr			
1060	1065	1070	
Lys Pro Thr Ser Cys Ala Val Ile Leu His Ser Pro Ser Ala His Phe			
1075	1080	1085	
Thr Gly Arg Trp Asp Asp Arg Ser Cys Thr Glu Glu Thr His Gly Phe			
1090	1095	1100	
Ile Cys Gln Lys Gly Thr Asp Pro Ser Leu Ser Pro Ser Pro Ala Ala			
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Thr Pro Pro Ala Pro Gly Ala Glu Leu Ser Tyr Leu Asn His Thr Phe			
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Arg Leu Leu Gln Lys Pro Leu Arg Trp Lys Asp Ala Leu Leu Cys			
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Glu Ser Arg Asn Ala Ser Leu Ala His Val Pro Asp Pro Tyr Thr Gln			
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Ala Phe Leu Thr Gln Ala Ala Arg Gly Leu Gln Thr Pro Leu Trp Ile			
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Gly Leu Ala Ser Glu Glu Gly Ser Arg Arg Tyr Ser Trp Leu Ser Glu			
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Gly Gly Cys Ala Tyr Val Asp Val Asp Gly Thr Trp Arg Thr Thr Ser			
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Cys Asp Thr Lys Leu Gln Gly Ala Val Cys Gly Val Ser Arg Gly Pro			
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Pro Pro Arg Arg Ile Asn Tyr Arg Gly Ser Cys Pro Gln Gly Leu Ala			
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Asp Ser Ser Trp Ile Pro Phe Arg Glu His Cys Tyr Ser Phe His Met			
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Gly Gly Thr Val Leu Ser Ile Leu Asp Glu Met Glu Asn Val Phe Val			
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Trp Glu His Leu Gln Thr Ala Glu Ala Gln Ser Arg Gly Ala Trp Leu			
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Gly Met Asn Phe Asn Pro Lys Gly Gly Thr Leu Val Trp Gln Asp Asn			
1330	1335	1340	
Thr Ala Val Asn Tyr Ser Asn Trp Gly Pro Pro Gly Leu Gly Pro Ser			
1345	1350	1355	1360

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 1395 1400 1405
 Glu Ser Pro Val Ala Leu Val Val Val Leu Thr Ala Val Leu Leu Leu
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<210> 306
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 <212> DNA
 <213> Rat

<400> 306

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PEN's
CEN plus
with tagline # 25 (PEN3) + H 47 (PEN6) are G1, rascf are G3

Table 1. Previously characterized and novel Pan Endothelial Markers. The most abundant tags derived by summing the tags from Normal EC (N-EC's) and Tumor EC (T-EC's) SAGE libraries are listed in descending order. N-EC and T-EC SAGE libraries contained 88,684 and 88,688 SAGE tags respectively. For comparison, the corresponding number of SAGE tags found in cultured human umbilical vein endothelial cells (HUVEC), human dermal microvascular endothelial cells (HMVEC), and non-endothelial cell lines (Cell Lines) are shown. The HUVEC SAGE library contained 280,000 tags and the HMVEC library 111,000 tags. Non-endothelial cell lines consisted of 1.8x10⁶ tags derived from a total of 14 different cancer cell lines including colon, breast, lung, and pancreatic cancers, as well as one non-transformed keratinocyte cell line, two kidney epithelial cell lines, and normal monocytes. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parentheses. The sequence CATG precedes all tags and the 15th base (11th shown) was determined as previously described by Veilescu et al. (Nat Genet 1999 Dec;23(4):387-8).

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC Cell Lines	Description
1	CATATCATTA	247	501	130	87	2 angiotensin (ANG), IGFBP-7, IGFBP-7P1, Mac25, TAF1
2	TGCACTTCAG	328	141	0	0	0 hevin
3	TTTGCACCTT	165	84	191	115	4 connective tissue growth factor (CTGF, IGFBP-7P2)
4	CCCTGTCCG	131	104	1	1	0 ESTs
5	TTGCTGACTT	73	131	2	14	1 collagen, type VI, alpha 1
6	ACCATTGGATT	102	67	0	0	2 Interferon induced transmembrane protein 1 (IF-27, Leu 13)
7	ACACCTCTTC	104	44	60	62	2 guanine nucleotide binding protein 11
8	TTCTGCTCTG	71	67	118	72	0 von Willebrand factor
9	TCCCTGGCGA	68	68	3	13	3 cysteine-rich protein 2 (CRP-2, ESP-1, SmILIM)
10	TAATCCTCAAG	28	108	34	18	1 collagen, type XVIII, alpha 1
11	ATGTCCTTTCT	68	65	17	17	3 insulin-like growth factor-binding protein 4
12	GGGATAAAAGC	40	67	30	14	2 CD148 (S-Endo 1, P1H12, Muc18, MCAM, Mel-CAM)
13	TTAGTGTGCTA	38	69	9	13	0 SPARC (osteonectin, BM-40)
14	TTCTTCCAAAT	20	86	16	84	2 collagen, type IV, alpha 2
15	GTGCTAACGCC	24	74	0	10	2 collagen, type VI, alpha 2
16	GTTTAGGGATA	35	58	11	11	1 matrix Gla protein (MGP)
17	CCCTTTCACAC	52	33	0	0	0 ESTs, Weakly similar to HPBRI-7 protein
18	TGTTCTGGAGA	58	27	18	56	2 gap junction protein, alpha 1, 43kD (connexin 43)
19	AAGATCAAAGAT	34	50	2	4	1 actin, alpha 1, skeletal muscle / actin, alpha 2; smooth muscle, aorta
20	TCTCTGAGCAT	32	48	0	0	0 aggrecanase 1 (metalloproteinase with thrombospondin type 1 motifs, 4)
21	CAGGTTTCATA	22	56	0	0	0 small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAFQ)
22	GCACAAGTTCT	43	26	6	22	0 calcitonin receptor-like receptor activity modifying protein 2
23	AGCTTGTGGCC	45	23	0	0	0 calcitonin receptor-like receptor activity modifying protein 3
24	CTTCTGGATAA	13	54	12	0	0 cell division cycle 42 (GTP-binding protein, 25kD)
25	CAACATAATA	42	25	13	6	0 ESTs

G1

TEM's complete web table

Table 2. SAGE tags elevated in tumor endothelium. The top 46 tags with the highest tumor EC (T-EC's) to normal EC (N-EC's) tag ratios are listed in descending order. To calculate tag ratios, a value of 0.5 was assigned in cases where zero tags were observed. The SAGE libraries are the same as those listed in Table 1. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis. †; multiple tags for this gene are due to alternative polyadenylation sites.

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC Cell Lines	Description
1	GGGGCTGCCCA	0	28	0	2	ESTs, similarity to thrombomodulin <i>TEM1</i>
2	GATCTCCGTT	0	25	0	0	ESTs, similarity to rat Rhes ras-related protein <i>TEM2</i>
3	CATTTTTATCT	0	23	0	0	ESTs
4	CTTCTTTGAG	0	22	6	20	ESTs, similarity to JNK interacting protein-3 ^a (REIC)
5	TATTAACCTCT	0	21	1	3	ESTs, similarity to MMP-11 (stromelysin 3)
6	CAGGAGCCCC	0	16	2	0	MMP-2 (gelatinase A, 72kD type IV collagenase)
7	GGAAATGTCAA	0	31	53	22	ESTs
8	CCTGGTTCACT	0	15	0	0	ESTs
9	TTTTAAGAAC	0	14	1	4	collagen, type I, alpha 2, transcript A [†]
10	TTTGGGTTTCC	0	5	139	16	ESTs, similarity with sea squirt nitrogen <i>TEM3</i>
11	ATTTTGTATGA	0	13	0	4	ESTs, similarity with homeobox protein DLX-3 <i>TEM4</i>
12	ACTTTAGATGG	1	23	0	8	ESTs, similarity with collagen, type VI, alpha 3
13	GAGTGAGACCC	3	63	0	15	ESTs, Thy-1 cell surface antigen
14	GTACACACACC	0	10	0	0	ESTs / crystallin S
15	CCACAGGGGAT	2	38	0	2	ESTs, collagen, type III, alpha 1
16	TTAAAAGTCAC	1	19	1	1	ESTs, similarity with sea squirt nitrogen <i>TEM5</i>
17	ACAGACTGTTA	4	74	0	0	ESTs, similarity with homeobox protein DLX-3 <i>TEM4</i>
18	CCACTGCAAACC	1	18	0	1	ESTs, similarity with collagen, type I, alpha 2, transcript B [†]
19	CTATAGGAGAC	1	18	0	0	ESTs / pregnancy specific beta-1-glycoprotein 1
20	GTTCACAGAA	0	9	9	1	endo180 lectin
21	TACCACTCTCC	0	9	4	1	ESTs, Okfzp434G162 protein
22	GGCCCTTCTCT	1	17	3	2	bone morphogenic protein 1 (metalloprotease)
23	TTAAATAGCAC	2	33	0	0	ESTs, Okfzp434G162 protein
24	AGACATACTGA	1	16	1	0	ESTs, KIAA0672 gene product
25	TCCCCCAGGGAG	1	16	0	0	ESTs, KIAA0672 gene product
26	AGCCCCAAAGTG	0	8	8	ESTs, KIAA0672 gene product	
27	ACTACCATAAC	1	16	0	0	ESTs, KIAA0672 gene product
all	TACAATCGTT	0	8	8	ESTs, KIAA0672 gene product	

G3

				ESTs
29	TGGGTGAAAA	0	0	0
30	CATTATCCAA	0	0	0
31	AGAAACCACGG	0	0	0
32	ACCAAAACAC	0	0	0
33	TGAAATAAAC	0	0	0
34	TTTGGTTTCC	8	2	7
35	GTGGAGACGGG	6	0	3
36	TTTGTGTGTA	6	1	0
37	TTATGTTAAT	6	2	0
38	TGAAATGACC	15	14	0
39	TGAAATGACC	1	39	0
40	TGCCACACAGT	15	0	0
41	GATGAGGAGAC	3	0	0
42	ATCAAAGGTTT	3	0	0
43	AGTCACATAGT	2	23	0
44	TTCGGTTGGTC	1	11	0
45	CCCCACACGGG	4	45	0
46	GGCTTGCTTT	2	21	0
	ATCCCTTCCC	1	10	0
				peanut-like protein 1

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Table 3. Detection of transcripts in various tumor types by RT-PCR and *In situ* hybridization (ISH). The "+" sign indicates the presence of a robust RT-PCR product or strong positive staining of vessels by *In situ* hybridization. The ":" sign indicates an undetectable signal by *In situ* hybridization or an absent or barely detectable transcript by RT-PCR. The "+/-" sign indicates a very weak signal in a limited number vessels by *In situ* hybridization.

	TEM1	TEM3	TEM4	TEM5	TEM7	TEM8	TEM9	WIF	Hævin
RT-PCR	-	-	-	-	-	-	-	+	ND
	Colon Nor.	+	+	+	+	+	+	+	ND
Colon Tum.	-	-	-	-	-	-	-	+	+
	Colon Tum.	+	+	+	+	+	+	+	+
Liver Met.	+	+/-	+	+	+	+	+	+/-	ND
	Lung Tum.	+	ND	+	+	+	+	+	+
Brain Tum.	+	ND	ND	ND	+	ND	ND	+	+*
	Corpus Lut.	+	+	+	+	-	+	+	+
Wound	+	ND	+	ND	+/-	+/-	ND	+	+

* hævin was localized to both endothelial cells and malignant cells in brain tissue.
ND: not determined.

www.sagenet.org/langlois/table3.htm (to be posted upon publication)

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Table 9. SAGE tags elevated in normal endothelium. The top 46 tags with the highest normal EC (N-EC's) to tumor EC (T-EC's) tag ratios are listed in descending order. To calculate tag ratios, a value of 0.5 was assigned in cases where zero tags were observed. The SAGE libraries are the same as those listed in Table 1. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis.

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC Cell Lines	Description
1	TCTCACGGTCT	26	0	0	0	mucosal vascular addressin cell adhesion molecule 1
2	CTAGCGTTTT	19	0	4	14	serum deprivation response (phosphatidylserine-binding protein)
3	GTGGCTGACG	18	0	1	0	ESTs / intercellular adhesion molecule 4
4	CTCTAAAAAA	34	1	1	0	small inducible cytokine subfamily A (Cys-Cys), member 14
5	TGGGAAGAGG	16	0	3	4	ESTs
6	GTTTAAGGAT	16	0	0	0	ESTs
7	CTTGTGTTTG	15	0	58	32	endothelin 1 / ribosomal protein L27
8	ATTGCCAATC	14	0	0	4	TU3A protein
9	TGTTGAAAAA	21	1	0	0	selectin E (endothelial adhesion molecule 1)
10	ACAAAAAGGC	21	1	0	6	TU3A protein
11	AAGATGCACAC	21	1	1	1	phosphodiesterase 1 - nucleotide pyrophosphatase 2 (autotaxin)
12	GTAGAGGGAA	10	0	0	0	platelet/endothelial cell adhesion molecule (CD31 antigen)
13	TTGTTCAAGG	10	0	0	0	ESTs
14	CTCTTCAAAAAA	19	1	1	0	ESTs / small inducible cytokine subfamily A, member 14
15	TATTAATAATA	18	1	6	1	transforming growth factor, beta receptor II (70-80kD)
16	GAATTCCACCA	9	0	0	14	ESTs
17	AGGGAGAACT	9	0	0	0	small inducible cytokine subfamily A, member 14
18	ATATCTGAC	9	0	2	2	active BCR-related gene
19	TCAGTGACCAG	17	1	4	7	protein kinase C eta
20	GCAGAGTCCC	32	2	1	5	ESTs
21	TAAATACCTTG	8	0	2	0	ESTs (2 unigene clusters)
22	GTCACTAATT	8	0	1	0	ESTs
23	ATAACCTGCA	8	0	0	0	signalling lymphocytic activation molecule
24	TGCATCTGTGC	46	3	1	1	ESTs / glycogenin 2
25	TAAAGGCACA	15	1	4	3	LIM binding domain 2
26	GACGGGGGCT	73	5	11	7	claudin 5
27	ACTCCGGGT	14	1	0	8	ESTs

					GTP-binding protein
28	CTTCTCACCT	27	2	3	0
29	TCGTGCTTG	13	1	0	ESTs
30	GAGCAGTGCT	13	1	4	feline sarcoma viral (v-fes) - Fujinami avian sarcoma viral (v-fps) homolog
31	CTCTAAAAAA	10	1	0	ESTs
32	GAAACCCGGT	10	1	0	phospholipase C, beta 4
33	AACACAGTGC	10	1	7	ESTs
				15	1

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